HUMAN xiap

```
                    gaaaaggtggacaagtcctaatttcaagagaagatgacttttaacagttttgaaggatct
SEQ ID NO:3       1 ---------+---------+---------+---------+---------+---------+ 60
SEQ ID NO:4 a                                     M  T  F  N  S  F  E  G  S   -

                    aaaacttgtgtacctgcagacatcaataaggaagaagaatttgtagaagagtttaataga
                 61 ---------+---------+---------+---------+---------+---------+ 120
               a    K  T  C  V  P  A  D  I  N  K  E  E  E  F  V  E  E  F  N  R   -

                    ttaaaaacttttgctaattttccaagtggtagtcctgtttcagcatcaacactggcacga
                121 ---------+---------+---------+---------+---------+---------+ 180
               a    L  K  T  F  A  N  F  P  S  G  S  P  V  S  A  S  T  L  A  R   -

                    gcagggtttctttatactggtgaaggagataccgtgcggtgctttagttgtcatgcagct
                181 ---------+---------+---------+---------+---------+---------+ 240
               a    A  G  F  L  Y  T  G  E  G  D  T  V  R  C  F  S  C  H  A  A   -

                    gtagatagatggcaatatggagactcagcagttggaagacacaggaaagtatccccaaat
                241 ---------+---------+---------+---------+---------+---------+ 300
               a    V  D  R  W  Q  Y  G  D  S  A  V  G  R  H  R  K  V  S  P  N   -

                    tgcagatttatcaacggcttttatcttgaaaatagtgccacgcagtctacaaattctggt
                301 ---------+---------+---------+---------+---------+---------+ 360
               a    C  R  F  I  N  G  F  Y  L  E  N  S  A  T  Q  S  T  N  S  G   -
```

OIPE IAP55 OCT 27 2005 PATENT & TRADEMARK OFFICE

Fig. 1 (page 1 of 7)

HUMAN xiap

```
    atccagaatggtcagtacaaagttgaaaactatctgggaagcagagatcattttgcctta
361 ---------+---------+---------+---------+---------+---------+---------+ 420
a       I  Q  N  G  Q  Y  K  V  E  N  Y  L  G  S  R  D  H  F  A  L  -

    gacaggccatctgagacacatgcagactatcttttgagaactgggcaggttgtagatata
421 ---------+---------+---------+---------+---------+---------+---------+ 480
a       D  R  P  S  E  T  H  A  D  Y  L  L  R  T  G  Q  V  V  D  I  -

    tcagacaccatatacccgaggaaccctgccatgtattgtgaagaagctagattaaagtcc
481 ---------+---------+---------+---------+---------+---------+---------+ 540
a       S  D  T  I  Y  P  R  N  P  A  M  Y  C  E  E  A  R  L  K  S  -

    tttcagaactggccagactatgctcacctaaccccaagagagttagcaagtgctggactc
541 ---------+---------+---------+---------+---------+---------+---------+ 600
a       F  Q  N  W  P  D  Y  A  H  L  T  P  R  E  L  A  S  A  G  L  -

    tactacacaggtattggtgaccaagtgcagtgcttttgttgtggtggaaaactgaaaaat
601 ---------+---------+---------+---------+---------+---------+---------+ 660
a       Y  Y  T  G  I  G  D  Q  V  Q  C  F  C  C  G  G  K  L  K  N  -

    tgggaaccttgtgatcgtgcctggtcagaacacaggcgacactttcctaattgcttctttt
661 ---------+---------+---------+---------+---------+---------+---------+ 720
a       W  E  P  C  D  R  A  W  S  E  H  R  R  H  F  P  N  C  F  F  -
```

Fig. 1 (page 2 of 7)

HUMAN xiap

```
      gttttgggccggaatcttaatattcgaagtgaatctgatgctgtgagttctgataggaat
  721 ---------+---------+---------+---------+---------+---------+ 780
a       V  L  G  R  N  L  N  I  R  S  E  S  D  A  V  S  S  D  R  N  -

      ttcccaaattcaacaaatcttccaagaaatccatccatggcagattatgaagcacggatc
  781 ---------+---------+---------+---------+---------+---------+ 840
a       F  P  N  S  T  N  L  P  R  N  P  S  M  A  D  Y  E  A  R  I  -

      tttacttttgggacatggatatactcagttaacaaggagcagcttgcaagagctggattt
  841 ---------+---------+---------+---------+---------+---------+ 900
a       F  T  F  G  T  W  I  Y  S  V  N  K  E  Q  L  A  R  A  G  F  -

      tatgctttaggtgaaggtgataaagtaaagtgctttcactgtggaggagggctaactgat
  901 ---------+---------+---------+---------+---------+---------+ 960
a       Y  A  L  G  E  G  D  K  V  K  C  F  H  C  G  G  G  L  T  D  -

      tggaagcccagtgaagacccttgggaacaacatgctaaatggtatccagggtgcaaatat
  961 ---------+---------+---------+---------+---------+---------+ 1020
a       W  K  P  S  E  D  P  W  E  Q  H  A  K  W  Y  P  G  C  K  Y  -

      ctgttagaacagaagggacaagaatatataaacaatattcatttaactcattcacttgag
 1021 ---------+---------+---------+---------+---------+---------+ 1080
a       L  L  E  Q  K  G  Q  E  Y  I  N  N  I  H  L  T  H  S  L  E  -
```

Fig. 1 (page 3 of 7)

HUMAN xiap

```
       gagtgtctggtaagaactactgagaaaacaccatcactaactagaagaattgatgatacc
1081   ---------+---------+---------+---------+---------+---------+ 1140
a        E  C  L  V  R  T  T  E  K  T  P  S  L  T  R  R  I  D  D  T  -

       atcttccaaaatcctatggtacaagaagctatacgaatggggttcagtttcaaggacatt
1141   ---------+---------+---------+---------+---------+---------+ 1200
a        I  F  Q  N  P  M  V  Q  E  A  I  R  M  G  F  S  F  K  D  I  -

       aagaaaataatggaggaaaaaattcagatatctgggagcaactataaatcacttgaggtt
1201   ---------+---------+---------+---------+---------+---------+ 1260
a        K  K  I  M  E  E  K  I  Q  I  S  G  S  N  Y  K  S  L  E  V  -

       ctggttgcagatctagtgaatgctcagaaagacagtatgcaagatgagtcaagtcagact
1261   ---------+---------+---------+---------+---------+---------+ 1320
a        L  V  A  D  L  V  N  A  Q  K  D  S  M  Q  D  E  S  S  Q  T  -

       tcattacagaaagagattagtactgaagagcagctaaggcgcctgcaagaggagaagctt
1321   ---------+---------+---------+---------+---------+---------+ 1380
a        S  L  Q  K  E  I  S  T  E  E  Q  L  R  R  L  Q  E  E  K  L  -

       tgcaaaatctgtatggatagaaatattgctatcgttttgttccttgtggacatctagtc
1381   ---------+---------+---------+---------+---------+---------+ 1440
```

Fig. 1 (page 4 of 7)

HUMAN xiap

```
a          C  K  I  C  M  D  R  N  I  A  I  V  F  V  P  C  G  H  L  V  -

           acttgtaaacaatgtgctgaagcagttgacaagtgtcccatgtgctacacagtcattact
      1441 ---------+---------+---------+---------+---------+---------+ 1500

a          T  C  K  Q  C  A  E  A  V  D  K  C  P  M  C  Y  T  V  I  T  -

           ttcaagcaaaaaatttttatgtcttaatctaactctatagtaggcatgttatgttgttct
      1501 ---------+---------+---------+---------+---------+---------+ 1560

a          F  K  Q  K  I  F  M  S  *                                    -

           tattaccctgattgaatgtgtgatgtgaactgactttaagtaatcaggattgaattccat
      1561 ---------+---------+---------+---------+---------+---------+ 1620

a                                                                       -

           tagcatttgctaccaagtaggaaaaaaaatgtacatggcagtgttttagttggcaatata
      1621 ---------+---------+---------+---------+---------+---------+ 1680

a                                                                       -

           atctttgaatttcttgatttttcagggtattagctgtattatccatttttttttactgtta
      1681 ---------+---------+---------+---------+---------+---------+ 1740

a                                                                       -

           tttaattgaaaccatagactaagaataagaagcatcatactataactgaacacaatgtgt
      1741 ---------+---------+---------+---------+---------+---------+ 1800

a                                                                       -
```

Fig. 1 (page 5 of 7)

HUMAN xiap

```
     attcatagtatactgatttaatttctaagtgtaagtgaattaatcatctggatttttat
1801 ---------+---------+---------+---------+---------+---------+ 1860
a                                                                -

     tcttttcagataggcttaacaaatggagctttctgtatataaatgtggagattagagtta
1861 ---------+---------+---------+---------+---------+---------+ 1920
a                                                                -

     atctccccaatcacataatttgttttgtgtgaaaaaggaataaattgttccatgctggtg
1921 ---------+---------+---------+---------+---------+---------+ 1980
a                                                                -

     gaaagatagagattgtttttagaggttggttgttgtgttttaggattctgtccatttttct
1981 ---------+---------+---------+---------+---------+---------+ 2040
a                                                                -

     tgtaaagnnataaacacgnacntgtgcgaaatatntttgtaaagtgatttgccattnttg
2041 ---------+---------+---------+---------+---------+---------+ 2100
a                                                                -

     aaagcgtatttaatgatagaatactatcgagccaacatgtactgacatggaaagatgtca
2101 ---------+---------+---------+---------+---------+---------+ 2160
a                                                                -
```

Fig. 1 (page 6 of 7)

HUMAN xiap

```
     nagatatgttaagtgtaaaatgcaagtggcnnnacactatgtatagtctgagccagatca
2161 ---------+---------+---------+---------+---------+---------+ 2220
a                                                                  -

     aagtatgtatgttnttaatatgcatagaacnanagatttggaaagatatacaccaaactg
2221 ---------+---------+---------+---------+---------+---------+ 2280
a                                                                  -

     ttaaatgtggtttctcttcggggaggggggattgggggaggggccccagaggggtttta
2281 ---------+---------+---------+---------+---------+---------+ 2340
a                                                                  -

     naggggccttttcactttcnacttttttcattttgttctgttcgnatttttttataagtat
2341 ---------+---------+---------+---------+---------+---------+ 2400
a                                                                  -

     gtanaccccnaagggttttatggnaactaacatcagtaacctaacccccgtgactatcct
2401 ---------+---------+---------+---------+---------+---------+ 2460
a                                                                  -

     gtnctcttcctagggagctgtnttgtttcccacccaccacccttccctctgaacaaatgc
2461 ---------+---------+---------+---------+---------+---------+ 2520
a                                                                  -

     ctgagtgctggggcactttn
2521 ---------+---------+ 2540
a                        -
```

Fig. 1 (page 7 of 7)

HUMAN hiap-1

SEQ ID NO:5

```
          1 TCCTTGAGATGTATCAGTATAGGATTTAGGATCTCCATGTTGGAACTCTAAATGCATAGA
            ---------+---------+---------+---------+---------+---------+ 60
c                                                                         -

         61 AATGGAAATAATGGAAATTTTTCATTTTGGCTTTTCAGCCTAGTATTAAAACTGATAAAA
            ---------+---------+---------+---------+---------+---------+ 120
c                                                                         -

        121 GCAAAGCCATGCACAAAACTACCTCCCTAGAGAAAGGCTAGTCCCTTTTCTTCCCCATTC
            ---------+---------+---------+---------+---------+---------+ 180
c                                                                         -

        181 ATTTCATTATGAACATAGTAGAAAACAGCATATTCTTATCAAATTTGATGAAAAGCGCCA
            ---------+---------+---------+---------+---------+---------+ 240
SEQ ID NO:6 c         M  N  I  V  E  N  S  I  F  L  S  N  L  M  K  S  A  N -

        241 ACACGTTTGAACTGAAATACGACTTGTCATGTGAACTGTACCGAATGTCTACGTATTCCA
            ---------+---------+---------+---------+---------+---------+ 300
c         T  F  E  L  K  Y  D  L  S  C  E  L  Y  R  M  S  T  Y  S  T -

        301 CTTTTCCTGCTGGGGTTCCTGTCTCAGAAAGGAGTCTTGCTCGTGCTGGTTTCTATTACA
            ---------+---------+---------+---------+---------+---------+ 360
c         F  P  A  G  V  P  V  S  E  R  S  L  A  R  A  G  F  Y  Y  T -
```

Fig. 2 (page 1 of 8)

HUMAN hiap-1

```
      CTGGTGTGAATGACAAGGTCAAATGCTTCTGTTGTGGCCTGATGCTGGATAACTGGAAAA
  361 ---------+---------+---------+---------+---------+---------+ 420
C       G  V  N  D  K  V  K  C  F  C  C  G  L  M  L  D  N  W  K  R -

      GAGGAGACAGTCCTACTGAAAAGCATAAAAAGTTGTATCCTAGCTGCAGATTCGTTCAGA
  421 ---------+---------+---------+---------+---------+---------+ 480
C       G  D  S  P  T  E  K  H  K  K  L  Y  P  S  C  R  F  V  Q  S -

      GTCTAAATTCCGTTAACAACTTGGAAGCTACCTCTCAGCCTACTTTTCCTTCTTCAGTAA
  481 ---------+---------+---------+---------+---------+---------+ 540
C       L  N  S  V  N  N  L  E  A  T  S  Q  P  T  F  P  S  S  V  T -

      CACATTCCACACACTCATTACTTCCGGGTACAGAAAACAGTGGATATTTCCGTGGCTCTT
  541 ---------+---------+---------+---------+---------+---------+ 600
C       H  S  T  H  S  L  L  P  G  T  E  N  S  G  Y  F  R  G  S  Y -

      ATTCAAACTCTCCATCAAATCCTGTAAACTCCAGAGCAAATCAAGAATTTTCTGCCTTGA
  601 ---------+---------+---------+---------+---------+---------+ 660
C       S  N  S  P  S  N  P  V  N  S  R  A  N  Q  E  F  S  A  L  M -

      TGAGAAGTTCCTACCCCTGTCCAATGAATAACGAAAATGCCAGATTACTTACTTTTCAGA
  661 ---------+---------+---------+---------+---------+---------+ 720
C       R  S  S  Y  P  C  P  M  N  N  E  N  A  R  L  L  T  F  Q  T -
```

Fig. 2 (page 2 of 8)

HUMAN hiap-1

```
      CATGGCCATTGACTTTTCTGTCGCCAACAGATCTGGCACGAGCAGGCTTTTACTACATAG
  721 ---------+---------+---------+---------+---------+---------+ 780
C           W  P  L  T  F  L  S  P  T  D  L  A  R  A  G  F  Y  Y  I  G -

      GACCTGGAGACAGAGTGGCTTGCTTTGCCTGTGGTGGAAAATTGAGCAATTGGGAACCGA
  781 ---------+---------+---------+---------+---------+---------+ 840
C           P  G  D  R  V  A  C  F  A  C  G  G  K  L  S  N  W  E  P  K -

      AGGATAATGCTATGTCAGAACACCTGAGACATTTTCCCAAATGCCCATTTATAGAAAATC
  841 ---------+---------+---------+---------+---------+---------+ 900
C           D  N  A  M  S  E  H  L  R  H  F  P  K  C  P  F  I  E  N  Q -

      AGCTTCAAGACACTTCAAGATACACAGTTTCTAATCTGAGCATGCAGACACATGCAGCCC
  901 ---------+---------+---------+---------+---------+---------+ 960
C           L  Q  D  T  S  R  Y  T  V  S  N  L  S  M  Q  T  H  A  A  R -

      GCTTTAAAACATTCTTTAACTGGCCCTCTAGTGTTCTAGTTAATCCTGAGCAGCTTGCAA
  961 ---------+---------+---------+---------+---------+---------+ 1020
C           F  K  T  F  F  N  W  P  S  S  V  L  V  N  P  E  Q  L  A  S -

      GTGCGGGTTTTTATTATGTGGGTAACAGTGATGATGTCAAATGCTTTTGCTGTGATGGTG
 1021 ---------+---------+---------+---------+---------+---------+ 1080
C           A  G  F  Y  Y  V  G  N  S  D  D  V  K  C  F  C  C  D  G  G -
```

Fig. 2 (page 3 of 8)

HUMAN hiap-1

```
     GACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGTTCAACATGCCAAGTGGTTTCCAA
1081 ---------+---------+---------+---------+---------+---------+ 1140
C          L  R  C  W  E  S  G  D  D  P  W  V  Q  H  A  K  W  F  P  R -

     GGTGTGAGTACTTGATAAGAATTAAAGGACAGGAGTTCATCCGTCAAGTTCAAGCCAGTT
1141 ---------+---------+---------+---------+---------+---------+ 1200
C          C  E  Y  L  I  R  I  K  G  Q  E  F  I  R  Q  V  Q  A  S  Y -

     ACCCTCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCCAGGAGATGAAAATGCAG
1201 ---------+---------+---------+---------+---------+---------+ 1260
C          P  H  L  L  E  Q  L  L  S  T  S  D  S  P  G  D  E  N  A  E -

     AGTCATCAATTATCCATTTGGAACCTGGAGAAGACCATTCAGAAGATGCAATCATGATGA
1261 ---------+---------+---------+---------+---------+---------+ 1320
C          S  S  I  I  H  L  E  P  G  E  D  H  S  E  D  A  I  M  M  N -

     ATACTCCTGTGATTAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCCTGGTAAAACAGA
1321 ---------+---------+---------+---------+---------+---------+ 1380
C          T  P  V  I  N  A  A  V  E  M  G  F  S  R  S  L  V  K  Q  T -

     CAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAATTATAGACTAGTCAATGATCTTGTGT
1381 ---------+---------+---------+---------+---------+---------+ 1440
C          V  Q  R  K  I  L  A  T  G  E  N  Y  R  L  V  N  D  L  V  L -
```

Fig. 2 (page 4 of 8)

HUMAN hiap-1

```
     TAGACTTACTCAATGCAGAAGATGAAATAAGGGAAGAGGAGAGAGAAAGAGCAACTGAGG
1441 ---------+---------+---------+---------+---------+---------+ 1500
C          D   L   L   N   A   E   D   E   I   R   E   E   E   R   E   R   A   T   E   E -

     AAAAAGAATCAAATGATTTATTATTAATCCGGAAGAATAGAATGGCACTTTTTCAACATT
1501 ---------+---------+---------+---------+---------+---------+ 1560
C          K   E   S   N   D   L   L   L   I   R   K   N   R   M   A   L   F   Q   H   L -

     TGACTTGTGTAATTCCAATCCTGGATAGTCTACTAACTGCCGGAATTATTAATGAACAAG
1561 ---------+---------+---------+---------+---------+---------+ 1620
C          T   C   V   I   P   I   L   D   S   L   L   T   A   G   I   I   N   E   Q   E -

     AACATGATGTTATTAAACAGAAGACACAGACGTCTTTACAAGCAAGAGAACTGATTGATA
1621 ---------+---------+---------+---------+---------+---------+ 1680
C          H   D   V   I   K   Q   K   T   Q   T   S   L   Q   A   R   E   L   I   D   T -

     CGATTTTAGTAAAAGGAAATATTGCAGCCACTGTATTCAGAAACTCTCTGCAAGAAGCTG
1681 ---------+---------+---------+---------+---------+---------+ 1740
C          I   L   V   K   G   N   I   A   A   T   V   F   R   N   S   L   Q   E   A   E -

     AAGCTGTGTTATATGAGCATTTATTTGTGCAACAGCACATAAAATATATTCCCACAGAAG
1741 ---------+---------+---------+---------+---------+---------+ 1800
C          A   V   L   Y   E   H   L   F   V   Q   Q   D   I   K   Y   I   P   T   E   D -
```

Fig. 2 (page 5 of 8)

HUMAN hiap-1

```
     ATGTTTCAGATCTACCAGTGGAAGAACAATTGCGGAGACTACCAGAAGAAAGAACATGTA
1801 ---------+---------+---------+---------+---------+---------+ 1860
c          V  S  D  L  P  V  E  E  Q  L  R  R  L  P  E  E  R  T  C  K -

     AAGTGTGTATGGACAAAGAAGTGTCCATAGTGTTTATTCCTTGTGGTCATCTAGTAGTAT
1861 ---------+---------+---------+---------+---------+---------+ 1920
c          V  C  M  D  K  E  V  S  I  V  F  I  P  C  G  H  L  V  V  C -

     GCAAAGATTGTGCTCCTTCTTTAAGAAAGTGTCCTATTTGTAGGAGTACAATCAAGGGTA
1921 ---------+---------+---------+---------+---------+---------+ 1980
c          K  D  C  A  P  S  L  R  K  C  P  I  C  R  S  T  I  K  G  T -

     CAGTTCGTACATTTCTTTCATGAAGAAGAACCAAAACATCGTCTAAACTTTAGAATTAAT
1981 ---------+---------+---------+---------+---------+---------+ 2040
c          V  R  T  F  L  S  *                                      -

     TTATTAAATGTATTATAACTTTAACTTTTATCCTAATTTGGTTTCCTTAAAATTTTTATT
2041 ---------+---------+---------+---------+---------+---------+ 2100
c                                                                  -

     TATTTACAACTCAAAAAACATTGTTTTGTGTAACATATTTATATATGTATCTAAACCATA
2101 ---------+---------+---------+---------+---------+---------+ 2160
c                                                                  -
```

Fig. 2 (page 6 of 8)

HUMAN hiap-1

```
     TGAACATATATTTTTTAGAAACTAAGAGAATGATAGGCTTTTGTTCTTATGAACGAAAAA
2161 ---------+---------+---------+---------+---------+---------+ 2220
c                                                                  -

     GAGGTAGCACTACAAACACAATATTCAATCCAAATTTCAGCATTATTGAAATTGTAAGTG
2221 ---------+---------+---------+---------+---------+---------+ 2280
c                                                                  -

     AAGTAAAACTTAAGATATTTGAGTTAACCTTTAAGAATTTTAAATATTTTGGCATTGTAC
2281 ---------+---------+---------+---------+---------+---------+ 2340
c                                                                  -

     TAATACCGGGAACATGAAGCCAGGTGTGGTGGTATGTACCTGTAGTCCCAGGCTGAGGCA
2341 ---------+---------+---------+---------+---------+---------+ 2400
c                                                                  -

     AGAGAATTACTTGAGCCCAGGAGTTTGAATCCATCCTGGGCAGCATACTGAGACCCTGCC
2401 ---------+---------+---------+---------+---------+---------+ 2460
c                                                                  -

     TTTAAAAACXAACAGXACCAAAXCCAAACACCAGGGACACATTTCTCTGTCTTTTTTGAT
2461 ---------+---------+---------+---------+---------+---------+ 2520
c                                                                  -
```

Fig. 2 (page 7 of 8)

HUMAN hiap-1

```
     CAGTGTCCTATACATCGAAGGTGTGCATATATGTTGAATCACATTTTAGGGACATGGTGT
2521 ---------+---------+---------+---------+---------+---------+ 2580

c                                                                -

     TTTTATAAAGAATTCTGTGAGXAAAAATTTAATAAAGCAACCXAAATTACTCTTAAAAAA
2581 ---------+---------+---------+---------+---------+---------+ 2640

c                                                                -

     AAAAAAAAAAAAAAAACTCGAGGGGCCCGTACCAAT
2641 ---------+---------+---------+------ 2676

c                                        -
```

Fig. 2 (page 8 of 8)

HUMAN hiap-2

SEQ ID NO:7

```
          1 TTAGGTTACCTGAAAGAGTTACTACAACCCCAAAGAGTTGTGTTCTAAGTAGTATCTTGG
            ---------+---------+---------+---------+---------+---------+ 60
a                                                                         -

         61 TAATTCAGAGAGATACTCATCCTACCTGAATATAAACTGAGATAAATCCAGTAAAGAAAG
            ---------+---------+---------+---------+---------+---------+ 120
a                                                                         -

        121 TGTAGTAAATTCTACATAAGAGTCTATCATTGATTTCTTTTTGTGGTGGAAATCTTAGTT
            ---------+---------+---------+---------+---------+---------+ 180
a                                                                         -

        181 CATGTGAAGAAATTTCATGTGAATGTTTTAGCTATCAAACAGTACTGTCACCTACTCATG
            ---------+---------+---------+---------+---------+---------+ 240
a                                                                   M     -

        241 CACAAAACTGCCTCCCAAAGACTTTTCCCAGGTCCCTCGTATCAAAACATTAAGAGTATA
            ---------+---------+---------+---------+---------+---------+ 300
SEQ ID NO:8 a       H  K  T  A  S  Q  R  L  F  P  G  P  S  Y  Q  N  I  K  S  I   -

        301 ATGGAAGATAGCACGATCTTGTCAGATTGGACAAACAGCAACAAACAAAAAATGAAGTAT
            ---------+---------+---------+---------+---------+---------+ 360
a       M  E  D  S  T  I  L  S  D  W  T  N  S  N  K  Q  K  M  K  Y   -
```

Fig. 3 (page 1 of 7)

HUMAN hiap-2

```
     GACTTTTCCTGTGAACTCTACAGAATGTCTACATATTCAACTTTCCCCGCCGGGGTGCCT
361  ---------+---------+---------+---------+---------+---------+ 420
a        D   F   S   C   E   L   Y   R   M   S   T   Y   S   T   F   P   A   G   V   P   -

     GTCTCAGAAAGGAGTCTTGCTCGTGCTGGTTTTTATTATACTGGTGTGAATGACAAGGTC
421  ---------+---------+---------+---------+---------+---------+ 480
a        V   S   E   R   S   L   A   R   A   G   F   Y   Y   T   G   V   N   D   K   V   -

     AAATGCTTCTGTTGTGGCCTGATGCTGGATAACTGGAAACTAGGAGACAGTCCTATTCAA
481  ---------+---------+---------+---------+---------+---------+ 540
a        K   C   F   C   C   G   L   M   L   D   N   W   K   L   G   D   S   P   I   Q   -

     AAGCATAAACAGCTATATCCTAGCTGTAGCTTTATTCAGAATCTGGTTTCAGCTAGTCTG
541  ---------+---------+---------+---------+---------+---------+ 600
a        K   H   K   Q   L   Y   P   S   C   S   F   I   Q   N   L   V   S   A   S   L   -

     GGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTTTGCACATTCATTATCTCCC
601  ---------+---------+---------+---------+---------+---------+ 660
a        G   S   T   S   K   N   T   S   P   M   R   N   S   F   A   H   S   L   S   P   -

     ACCTTGGAACATAGTAGCTTGTTCAGTGGTTCTTACTCCAGCCTTCCTCCAAACCCTCTT
661  ---------+---------+---------+---------+---------+---------+ 720
a        T   L   E   H   S   S   L   F   S   G   S   Y   S   S   L   P   P   N   P   L   -
```

Fig. 3 (page 2 of 7)

HUMAN hiap-2

```
      AATTCTAGAGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCCTACAGTTATGCAATG
  721 ---------+---------+---------+---------+---------+---------+ 780
a       N  S  R  A  V  E  D  I  S  S  S  R  T  N  P  Y  S  Y  A  M  -

      AGTACTGAAGAAGCCAGATTTCTTACCTACCATATGTGGCCATTAACTTTTTTGTCACCA
  781 ---------+---------+---------+---------+---------+---------+ 840
a       S  T  E  E  A  R  F  L  T  Y  H  M  W  P  L  T  F  L  S  P  -

      TCAGAATTGGCAAGAGCTGGTTTTTATTATATAGGACCTGGAGATAGGGTAGCCTGCTTT
  841 ---------+---------+---------+---------+---------+---------+ 900
a       S  E  L  A  R  A  G  F  Y  Y  I  G  P  G  D  R  V  A  C  F  -

      GCCTGTGGTGGGAAGCTCAGTAACTGGGAACCAAAGGATGATGCTATGTCAGAACACCGG
  901 ---------+---------+---------+---------+---------+---------+ 960
a       A  C  G  G  K  L  S  N  W  E  P  K  D  D  A  M  S  E  H  R  -

      AGGCATTTTCCCAACTGTCCATTTTTGGAAAATTCTCTAGAAACTCTGAGGTTTAGCATT
  961 ---------+---------+---------+---------+---------+---------+ 1020
a       R  H  F  P  N  C  P  F  L  E  N  S  L  E  T  L  R  F  S  I  -

      TCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTTATGTACTGGCCATCT
 1021 ---------+---------+---------+---------+---------+---------+ 1080
a       S  N  L  S  M  Q  T  H  A  A  R  M  R  T  F  M  Y  W  P  S  -
```

Fig. 3 (page 3 of 7)

HUMAN hiap-2

```
     AGTGTTCCAGTTCAGCCTGAGCAGCTTGCAAGTGCTGGTTTTTATTATGTGGGTCGCAAT
1081 ---------+---------+---------+---------+---------+---------+ 1140
a        S  V  P  V  Q  P  E  Q  L  A  S  A  G  F  Y  Y  V  G  R  N  -

     GATGATGTCAAATGCTTTGGTTGTGATGGTGGCTTGAGGTGTTGGGAATCTGGAGATGAT
1141 ---------+---------+---------+---------+---------+---------+ 1200
a        D  D  V  K  C  F  G  C  D  G  G  L  R  C  W  E  S  G  D  D  -

     CCATGGGTAGAACATGCCAAGTGGTTTCCAAGGTGTGAGTTCTTGATACGAATGAAAGGC
1201 ---------+---------+---------+---------+---------+---------+ 1260
a        P  W  V  E  H  A  K  W  F  P  R  C  E  F  L  I  R  M  K  G  -

     CAAGAGTTTGTTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAACAGCTGTTGTCA
1261 ---------+---------+---------+---------+---------+---------+ 1320
a        Q  E  F  V  D  E  I  Q  G  R  Y  P  H  L  L  E  Q  L  L  S  -

     ACTTCAGATACCACTGGAGAAGAAAATGCTGACCCACCAATTATTCATTTTGGACCTGGA
1321 ---------+---------+---------+---------+---------+---------+ 1380
a        T  S  D  T  T  G  E  E  N  A  D  P  P  I  I  H  F  G  P  G  -

     GAAAGTTCTTCAGAAGATGCTGTCATGATGAATACACCTGTGGTTAAATCTGCCTTGGAA
1381 ---------+---------+---------+---------+---------+---------+ 1440
a        E  S  S  S  E  D  A  V  M  M  N  T  P  V  V  K  S  A  L  E  -
```

Fig. 3 (page 4 of 7)

HUMAN hiap-2

```
      ATGGGCTTTAATAGAGACCTGGTGAAACAAACAGTTCTAAGTAAAATCCTGACAACTGGA
1441  ---------+---------+---------+---------+---------+---------+ 1500

a       M  G  F  N  R  D  L  V  K  Q  T  V  L  S  K  I  L  T  T  G  -

      GAGAACTATAAAACAGTTAATGATATTGTGTCAGCACTTCTTAATGCTGAAGATGAAAAA
1501  ---------+---------+---------+---------+---------+---------+ 1560

a       E  N  Y  K  T  V  N  D  I  V  S  A  L  L  N  A  E  D  E  K  -

      AGAGAAGAGGAGAAGGAAAAACAAGCTGAAGAAATGGCATCAGATGATTTGTCATTAATT
1561  ---------+---------+---------+---------+---------+---------+ 1620

a       R  E  E  E  K  E  K  Q  A  E  E  M  A  S  D  D  L  S  L  I  -

      CGGAAGAACAGAATGGCTCTCTTTCAACAATTGACATGTGTGCTTCCTATCCTGGATAAT
1621  ---------+---------+---------+---------+---------+---------+ 1680

a       R  K  N  R  M  A  L  F  Q  Q  L  T  C  V  L  P  I  L  D  N  -

      CTTTTAAAGGCCAATGTAATTAATAAACAGGAACATGATATTATTAAACAAAAAACACAG
1681  ---------+---------+---------+---------+---------+---------+ 1740

a       L  L  K  A  N  V  I  N  K  Q  E  H  D  I  I  K  Q  K  T  Q  -

      ATACCTTTACAAGCGAGAGAACTGATTGATACCATTTGGGTTAAAGGAAATGCTGCGGCC
1741  ---------+---------+---------+---------+---------+---------+ 1800

a       I  P  L  Q  A  R  E  L  I  D  T  I  W  V  K  G  N  A  A  A  -
```

Fig. 3 (page 5 of 7)

HUMAN hiap-2

```
     AACATCTTCAAAAACTGTCTAAAAGAAATTGACTCTACATTGTATAAGAACTTATTTGTG
1801 ---------+---------+---------+---------+---------+---------+ 1860

a       N  I  F  K  N  C  L  K  E  I  D  S  T  L  Y  K  N  L  F  V  -

     GATAAGAATATGAAGTATATTCCAACAGAAGATGTTTCAGGTCTGTCACTGGAAGAACAA
1861 ---------+---------+---------+---------+---------+---------+ 1920

a       D  K  N  M  K  Y  I  P  T  E  D  V  S  G  L  S  L  E  E  Q  -

     TTGAGGAGGTTGCAAGAAGAACGAACTTGTAAAGTGTGTATGGACAAAGAAGTTTCTGTT
1921 ---------+---------+---------+---------+---------+---------+ 1980

a       L  R  R  L  Q  E  E  R  T  C  K  V  C  M  D  K  E  V  S  V  -

     GTATTTATTCCTTGTGGTCATCTGGTAGTATGCCAGGAATGTGCCCCTTCTCTAAGAAAA
1981 ---------+---------+---------+---------+---------+---------+ 2040

a       V  F  I  P  C  G  H  L  V  V  C  Q  E  C  A  P  S  L  R  K  -

     TGCCCTATTTGCAGGGGTATAATCAAGGGTACTGTTCGTACATTTCTCTCTTAAAGAAAA
2041 ---------+---------+---------+---------+---------+---------+ 2100

a       C  P  I  C  R  G  I  I  K  G  T  V  R  T  F  L  S  *     -

     ATAGTCTATATTTTAACCTGCATAAAAAGGTCTTTAAAATATTGTTGAACACTTGAAGCC
2101 ---------+---------+---------+---------+---------+---------+ 2160

                                                                  -
a
```

Fig. 3 (page 6 of 7)

HUMAN hiap-2

```
     ATCTAAAGTAAAAAGGGAATTATGAGTTTTTCAATTAGTAACATTCATGTTCTAGTCTGC
2161 ---------+---------+---------+---------+---------+---------+ 2220

a                                                                -

     TTTGGTACTAATAATCTTGTTTCTGAAAAGATGGTATCATATATTTAATCTTAATCTGTT
2221 ---------+---------+---------+---------+---------+---------+ 2280

a                                                                  -

     TATTTACAAGGGAAGATTTATGTTTGGTGAACTATATTAGTATGTATGTGTACCTAAGGG
2281 ---------+---------+---------+---------+---------+---------+ 2340

a                                                                -

     AGTAGCGTCXCTGCTTGTTATGCATCATTTCAGGAGTTACTGGATTTGTTGTTCTTTCAG
2341 ---------+---------+---------+---------+---------+---------+ 2400

a                                                                -

     AAAGCTTTGAAXACTAAATTATAGTGTAGAAAAGAACTGGAAACCAGGAACTCTGGAGTT
2401 ---------+---------+---------+---------+---------+---------+ 2460

a                                                                -

     CATCAGAGTTATGGTGCCGAATTGTCTTTGGTGCTTTTCACTTGTGTTTTAAAATAAGGA
2461 ---------+---------+---------+---------+---------+---------+ 2520

a                                                                -

     TTTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTGCTTTAAAAAG
2521 ---------+---------+---------+---------+---------+---------+ 2580

a                                                                -
```

Fig. 3 (page 7 of 7)

MOUSE xiap

SEQ ID NO:9

```
          1 GACACTCTGCTGGGCGGCGGGCCGCCCTCCTCCGGGACCTCCCCTCGGGAACCGTCGCCC
            ---------+---------+---------+---------+---------+---------+ 60
a                                                                         -

         61 GCGGCGCTTAGTTAGGACTGGAGTGCTTGGCGCGAAAAGGTGGACAAGTCCTATTTTCCA
            ---------+---------+---------+---------+---------+---------+ 120
a                                                                         -

        121 GAGAAGATGACTTTTAACAGTTTTGAAGGAACTAGAACTTTTGTACTTGCAGACACCAAT
            ---------+---------+---------+---------+---------+---------+ 180
SEQ ID NO:10 a        M   T   F   N   S   F   E   G   T   R   T   F   V   L   A   D   T   N   -

        181 AAGGATGAAGAATTTGTAGAAGAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGT
            ---------+---------+---------+---------+---------+---------+ 240
a       K   D   E   E   F   V   E   E   F   N   R   L   K   T   F   A   N   F   P   S   -

        241 AGTAGTCCTGTTTCAGCATCAACATTGGCGCGAGCTGGGTTTCTTTATACCGGTGAAGGA
            ---------+---------+---------+---------+---------+---------+ 300
a       S   S   P   V   S   A   S   T   L   A   R   A   G   F   L   Y   T   G   E   G   -

        301 GACACCGTGCAATGTTTCAGTTGTCATGCGGCAATAGATAGATGGCAGTATGGAGACTCA
            ---------+---------+---------+---------+---------+---------+ 360
a       D   T   V   Q   C   F   S   C   H   A   A   I   D   R   W   Q   Y   G   D   S   -
```

Fig. 4 (page 1 of 6)

MOUSE xiap

```
     GCTGTTGGAAGACACAGGAGAATATCCCCAAATTGCAGATTTATCAATGGTTTTTATTTT
 361 ---------+---------+---------+---------+---------+---------+ 420
a        A  V  G  R  H  R  R  I  S  P  N  C  R  F  I  N  G  F  Y  F   -

     GAAAATGGTGCTGCACAGTCTACAAATCCTGGTATCCAAAATGGCCAGTACAAATCTGAA
 421 ---------+---------+---------+---------+---------+---------+ 480
a        E  N  G  A  A  Q  S  T  N  P  G  I  Q  N  G  Q  Y  K  S  E   -

     AACTGTGTGGGAAATAGAAATCCTTTTGCCCCTGACAGGCCACCTGAGACTCATGCTGAT
 481 ---------+---------+---------+---------+---------+---------+ 540
a        N  C  V  G  N  R  N  P  F  A  P  D  R  P  P  E  T  H  A  D   -

     TATCTCTTGAGAACTGGACAGGTTGTAGATATTTCAGACACCATATACCCGAGGAACCCT
 541 ---------+---------+---------+---------+---------+---------+ 600
a        Y  L  L  R  T  G  Q  V  V  D  I  S  D  T  I  Y  P  R  N  P   -

     GCCATGTGTAGTGAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGGACTATGCTCAT
 601 ---------+---------+---------+---------+---------+---------+ 660
a        A  M  C  S  E  E  A  R  L  K  S  F  Q  N  W  P  D  Y  A  H   -

     TTAACCCCCAGAGAGTTAGCTAGTGCTGGCCTCTACTACACAGGGGCTGATGATCAAGTG
 661 ---------+---------+---------+---------+---------+---------+ 720
a        L  T  P  R  E  L  A  S  A  G  L  Y  Y  T  G  A  D  D  Q  V   -
```

Fig. 4 (page 2 of 6)

MOUSE xiap

```
      CAATGCTTTTGTTGTGGGGGAAAACTGAAAAATTGGGAACCCTGTGATCGTGCCTGGTCA
  721 ---------+---------+---------+---------+---------+---------+ 780
a       Q  C  F  C  C  G  G  K  L  K  N  W  E  P  C  D  R  A  W  S  -

      GAACACAGGAGACACTTTCCCAATTGCTTTTTTGTTTTGGGCCGGAACGTTAATGTTCGA
  781 ---------+---------+---------+---------+---------+---------+ 840
a       E  H  R  R  H  F  P  N  C  F  F  V  L  G  R  N  V  N  V  R  -

      AGTGAATCTGGTGTGAGTTCTGATAGGAATTTCCCAAATTCAACAAACTCTCCAAGAAAT
  841 ---------+---------+---------+---------+---------+---------+ 900
a       S  E  S  G  V  S  S  D  R  N  F  P  N  S  T  N  S  P  R  N  -

      CCAGCCATGGCAGAATATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTT
  901 ---------+---------+---------+---------+---------+---------+ 960
a       P  A  M  A  E  Y  E  A  R  I  V  T  F  G  T  W  I  Y  S  V  -

      AACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAG
  961 ---------+---------+---------+---------+---------+---------+ 1020
a       N  K  E  Q  L  A  R  A  G  F  Y  A  L  G  E  G  D  K  V  K  -

      TGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAG
 1021 ---------+---------+---------+---------+---------+---------+ 1080
a       C  F  H  C  G  G  G  L  T  D  W  K  P  S  E  D  P  W  D  Q  -
```

Fig. 4 (page 3 of 6)

MOUSE xiap

```
      CATGCTAAGTGCTACCCAGGGTGCAAATACCTATTGGATGAGAAGGGGCAAGAATATATA
1081  ---------+---------+---------+---------+---------+---------+ 1140
a         H  A  K  C  Y  P  G  C  K  Y  L  L  D  E  K  G  Q  E  Y  I  -

      AATAATATTCATTTAACCCATCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAAAAACA
1141  ---------+---------+---------+---------+---------+---------+ 1200
a         N  N  I  H  L  T  H  P  L  E  E  S  L  G  R  T  A  E  K  T  -

      CCACCGCTAACTAAAAAAATCGATGATACCATCTTCCAGAATCCTATGGTGCAAGAAGCT
1201  ---------+---------+---------+---------+---------+---------+ 1260
a         P  P  L  T  K  K  I  D  D  T  I  F  Q  N  P  M  V  Q  E  A  -

      ATACGAATGGGATTTAGCTTCAAGGACCTTAAGAAAACAATGGAAGAAAAAATCCAAACA
1261  ---------+---------+---------+---------+---------+---------+ 1320
a         I  R  M  G  F  S  F  K  D  L  K  K  T  M  E  E  K  I  Q  T  -

      TCCGGGAGCAGCTATCTATCACTTGAGGTCCTGATTGCAGATCTTGTGAGTGCTCAGAAA
1321  ---------+---------+---------+---------+---------+---------+ 1380
a         S  G  S  S  Y  L  S  L  E  V  L  I  A  D  L  V  S  A  Q  K  -

      GATAATACGGAGGATGAGTCAAGTCAAACTTCATTGCAGAAAGACATTAGTACTGAAGAG
1381  ---------+---------+---------+---------+---------+---------+ 1440
a         D  N  T  E  D  E  S  S  Q  T  S  L  Q  K  D  I  S  T  E  E  -
```

Fig. 4 (page 4 of 6)

MOUSE xiap

```
     CAGCTAAGGCGCCTACAAGAGGAGAAGCTTTCCAAAATCTGTATGGATAGAAATATTGCT
1441 ---------+---------+---------+---------+---------+---------+ 1500

a        Q  L  R  R  L  Q  E  E  K  L  S  K  I  C  M  D  R  N  I  A  -

     ATCGTTTTTTTTCCTTGTGGACATCTGGCCACTTGTAAACAGTGTGCAGAAGCAGTTGAC
1501 ---------+---------+---------+---------+---------+---------+ 1560

a        I  V  F  F  P  C  G  H  L  A  T  C  K  Q  C  A  E  A  V  D  -

     AAATGTCCCATGTGCTACACCGTCATTACGTTCAACCAAAAAATTTTTATGTCTTAGTGG
1561 ---------+---------+---------+---------+---------+---------+ 1620

a        K  C  P  M  C  Y  T  V  I  T  F  N  Q  K  I  F  M  S  *     -

     GGCACCACATGTTATGTTCTTCTTGCTCTAATTGAATGTGTAATGGGAGCGAACTTTAAG
1621 ---------+---------+---------+---------+---------+---------+ 1680

a                                                                  -

     TAATCCTGCATTTGCATTCCATTAGCATCCTGCTGTTTCCAAATGGAGACCAATGCTAAC
1681 ---------+---------+---------+---------+---------+---------+ 1740

a                                                                  -

     AGCACTGTTTCCGTCTAAACATTCAATTTCTGGATCTTTCGAGTTATCAGCTGTATCATT
1741 ---------+---------+---------+---------+---------+---------+ 1800

a                                                                  -
```

Fig. 4 (page 5 of 6)

MOUSE xiap

```
     TAGCCAGTGTTTTACTCGATTGAAACCTTAGACAGAGAAGCATTTTATAGCTTTTCACAT
1801 ---------+---------+---------+---------+---------+---------+ 1860

a                                                                -

     GTATATTGGTAGTACACTGACTTGATTTCTATATGTAAGTGAATTCATCACCTGCATGTT
1861 ---------+---------+---------+---------+---------+---------+ 1920

a                                                                -

     TCATGCCTTTTGCATAAGCTTAACAAATGGAGTGTTCTGTATAAGCATGGAGATGTGATG
1921 ---------+---------+---------+---------+---------+---------+ 1980

a                                                                -

     GAATCTGCCCAATGACTTTAATTGGCTTATTGTAAACACGGAAAGAACTGCCCCACGCTG
1981 ---------+---------+---------+---------+---------+---------+ 2040

a                                                                -

     CTGGGAGGATAAAGATTGTTTTAGATGCTCACTTCTGTGTTTTAGGATTCTGCCCATTTA
2041 ---------+---------+---------+---------+---------+---------+ 2100
```

Fig. 4 (page 6 of 6)

M-hiap-1

```
SEQ ID NO:39      GAATTCCGGGAGACCTACACCCCCGGAGATCAGAGGTCATTGCTGGCGTTCAGAGCCTAG
                  --------+--------+--------+--------+--------+--------+--------
                1 GAAGTGGGCTGCGGTATCAGCCTAGCAGTAAAACCGACCAGAAGCCATGCACAAAACTAC  60
                  --------+--------+--------+--------+--------+--------+--------
               61 ATCCCCAGAGAAAGACTTGTCCCTTCCCCTCCCTGTCATCTCACCATGAACATGGTTCAA 120
                  --------+--------+--------+--------+--------+--------+--------
              121                                                 M  N  M  V  Q  -
SEQ ID NO:40

                  GACAGCGCCTTTCTAGCCAAGCTGATGAAGAGTGCTGACACCTTTGAGTTGAAGTATGAC
                  +-------+--------+--------+--------+--------+--------+--------
              181 D  S  A  F  L  A  K  L  M  K  S  A  D  T  F  E  L  K  Y  D  -

                  TTTTCCTGTGAGCTGTACCGATTGTCCACGTATTCAGCTTTTCCCAGGGGAGTTCCTGTG
                  +-------+--------+--------+--------+--------+--------+--------
              241 F  S  C  E  L  Y  R  L  S  T  Y  S  A  F  D  R  G  V  P  V  -

                  TCAGAAAGGAGTCTGGCTCGTGCTGGCTTTTACTACACTGGTGCCAATGACAAGGTCAAG
                  +-------+--------+--------+--------+--------+--------+--------
              301 S  E  R  S  L  A  R  A  G  F  Y  Y  T  G  A  N  D  K  V  K  -

                  TGCTTCTGCTGTGGCCTGATGCTAGACAACTGGAAACAAGGGGACAGTCCCATGGAGAAG
                  +-------+--------+--------+--------+--------+--------+--------
              361 C  F  C  C  G  L  M  L  D  N  W  K  Q  G  D  S  P  M  E  K  -
```

Fig. 5 (page 1 of 6)

M-hiap-1

```
    CACAGAAAGTTGTACCCCAGCTGCAACTTTGTACAGACTTTGAATCCAGCCAACAGTCTG
421 ---------+---------+---------+---------+---------+---------+ 480
    H  R  K  L  Y  P  S  C  N  F  V  Q  T  L  N  P  A  N  S  L   -

    GAAGCTAGTCCTCGGCCTTCTCTTCCTTCCACGGCGATGAGCACCATGCCTTTGAGCTTT
481 ---------+---------+---------+---------+---------+---------+ 540
    E  A  S  P  R  P  S  L  P  S  T  A  M  S  T  M  P  L  S  F   -

    GCAAGTTCTGAGAATACTGGCTATTTCAGTGGCTCTTACTCGAGCTTTCCCTCAGACCCT
541 ---------+---------+---------+---------+---------+---------+ 600
    A  S  S  E  N  T  G  Y  F  S  G  S  Y  S  S  F  P  S  D  P   -

    GTGAACTTCCGAGCAAATCAAGATTGTCCTGCTTTGAGCACAAGTCCCTACCACTTTGCA
601 ---------+---------+---------+---------+---------+---------+ 660
    V  N  F  R  A  N  Q  D  C  P  A  L  S  T  S  P  Y  H  F  A   -

    ATGAACACAGAGAAGGCCAGATTACTCACCTATGAAACATGGCCATTGTCTTTTCTGTCA
661 ---------+---------+---------+---------+---------+---------+ 720
    M  N  T  E  K  A  R  L  L  T  Y  E  T  W  P  L  S  F  L  S   -

    CCAGCAAAGCTGGCCAAAGCAGGCTTCTACTACATAGGACCTGGAGATAGAGTGGCCTGC
721 ---------+---------+---------+---------+---------+---------+ 780
    P  A  K  L  A  K  A  G  F  Y  Y  I  G  P  G  D  R  V  A  C   -
```

Fig. 5 (page 2 of 6)

M-hiap-1

```
    TTTGCGTGCGATGGGAAACTGAGCAACTGGGAACGTAAGGATGATGCTATGTCAGAGCAC
781 ---------+---------+---------+---------+---------+---------+ 840
    F  A  C  D  G  K  L  S  N  W  E  R  K  D  D  A  M  S  E  H   -

    CAGAGGCATTTCCCCAGCTGTCCGTTCTTALLkGACTTGGGTCAGTCTGCTTCGAGATAC
841 ---------+---------+---------+---------+---------+---------+ 900
    Q  R  H  F  P  S  C  P  F  L  K  D  L  G  Q  S  A  S  R  Y   -

    ACTGTCTCTAACCTGAGCATGCAGACACACGCAGCCCGTATTAGAACATTCTCTAACTGG
901 ---------+---------+---------+---------+---------+---------+ 960
    T  V  S  N  L  S  M  Q  T  H  A  A  R  I  R  T  F  S  N  W   -

    CCTTCTAGTGCACTAGTTCATTCCCAGGAACTTGCAAGTGCGGGCTTTTATTATACAGGA
961 ---------+---------+---------+---------+---------+---------+ 1020
    P  S  S  A  L  V  H  S  Q  E  L  A  S  A  G  F  Y  Y  T  G   -

    CACAGTGATGATGTCAAGTGTTTATGCTGTGATGGTGGGCTGAGGTGCTGGGAATCTGGA
1021 ---------+---------+---------+---------+---------+---------+ 1080
    H  S  D  D  V  K  C  L  C  C  D  G  G  L  R  C  W  E  S  G   -

    GATGACCCCTGGGTGGAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTTGCTCAGAATC
1081 ---------+---------+---------+---------+---------+---------+ 1140
    D  D  P  W  V  E  H  A  K  W  F  P  R  C  E  Y  L  L  R  I   -

    AAAGGCCAAGAATTTGTCAGCCAAGTTCAAGCTGGCTATCCTCATCTACTTGAGCAGCTA
1141 ---------+---------+---------+---------+---------+---------+ 1200
    K  G  Q  E  F  V  S  Q  V  Q  A  G  Y  P  H  L  L  E  Q  L   -
```

Fig. 5 (page 3 of 6)

M-hiap-1

```
     TTATCTACGTCAGACTCCCCAGAAGATGAGAATGCAGACGCAGCAATCGTGCATTTTGGC
1201 ---------+---------+---------+---------+---------+---------+ 1260
     L  S  T  S  D  S  P  E  D  E  N  A  D  A  A  I  V  H  F  G  -

     CCTGGAGAAAGTTCGGAAGATGTCGTCATGATGAGCACGCCTGTGGTTAAAGCAGCCTTG
1261 ---------+---------+---------+---------+---------+---------+ 1320
     P  G  E  S  S  E  D  V  V  M  M  S  T  P  V  V  K  A  A  L  -

     GAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTCAGTGGCAGATCCTGGCCACT
1321 ---------+---------+---------+---------+---------+---------+ 1380
     E  M  G  E  S  R  S  L  V  R  Q  T  V  Q  W  Q  I  L  A  T  -

     GGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATGCAGAAGACGAG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     G  E  N  Y  R  T  V  S  D  L  V  I  G  L  L  D  A  E  D  E  -

     ATGAGAGAGGAGCAGATGGAGCAGGCGGCCGAGGAGGAGGAGTCAGATGATCTAGCACTA
1441 ---------+---------+---------+---------+---------+---------+ 1500
     M  R  E  E  Q  M  E  Q  A  A  E  E  E  E  S  D  D  L  A  L  -

     ATCCGGAAGAACAAAATGGTGCTTTTCCAACATTTGACGTGTGTGACACCAATGCTGTAT
1501 ---------+---------+---------+---------+---------+---------+ 1560
     I  R  K  N  K  M  V  L  F  Q  H  L  T  C  V  T  P  M  L  Y  -
```

Fig. 5 (page 4 of 6)

M-hiap-1

```
     TGCCTCCTAAGTGCAAGGGCCATCACTGAACAGGAGTGCAATGCTGTGAAACAGAAACCA
1561 ---------+---------+---------+---------+---------+---------+ 1620
     C  L  L  S  A  R  A  I  T  E  Q  E  C  N  A  V  K  Q  K  P  -

     CACACCTTACAAGCAAGCACACTGATTGATACTGTGTTAGCAAAAGGAAACACTGCAGCA
1621 ---------+---------+---------+---------+---------+---------+ 1680
     H  T  L  Q  A  S  T  L  I  D  T  V  L  A  K  G  N  T  A  A  -

     ACCTCATTCAGAAACTCCCTTCGGGAAATTGACCCTGCGTTATACAGAGATATATTTGTG
1681 ---------+---------+---------+---------+---------+---------+ 1740
     T  S  F  R  N  S  L  R  E  I  D  P  A  L  Y  R  D  I  F  V  -

     CAACAGGACATTAGGAGTCTTCCCACAGATGACATTGCAGCTCTACCAATGGAAGAACAG
1741 ---------+---------+---------+---------+---------+---------+ 1800
     Q  Q  D  I  R  S  L  P  T  D  D  I  A  A  L  P  M  E  E  Q  -

     TTGCGGCCCCTCCCGGAGGACAGAATGTGTAAAGTGTGTATGGACCGAGAGGTATCCATC
1801 ---------+---------+---------+---------+---------+---------+ 1860
     L  R  P  L  P  E  D  R  M  C  K  V  C  M  D  R  E  V  S  I  -

     GTGTTCATTCCCTGTGGCCATCTGGTCGTGTGCAAAGACTGCGCTCCCTCTCTGAGGAAG
1861 ---------+---------+---------+---------+---------+---------+ 1920
     V  F  I  P  C  G  H  L  V  V  C  K  D  C  A  P  S  L  R  K  -
```

Fig. 5 (page 5 of 6)

M-hiap-1

```
     TGTCCCATCTGTAGAGGGACCATCAAGGGCACAGTGCGCACATTTCTCTCCTGAACAAGA
1921 ---------+---------+---------+---------+---------+---------+---------+ 1980
     C  P  I  C  R  G  T  I  K  G  T  V  R  T  F  L  S  *           -

     CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACTGTCACTCCCAGTTCCAT
1981 ---------+---------+---------+---------+---------+---------+---------+ 2040
     TCGGAACTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACkCACAAATATAAACAT
2041 ---------+---------+---------+---------+---------+---------+---------+ 2100
     GAAAAACTTTTGTCTGAAGTCAAGAATGAATGAATTACTTATATAATAATTTTAATTGGT
2101 ---------+---------+---------+---------+---------+---------+---------+ 2160
     TTCCTTAAAAGTGCTATTTGTTCCCAACTCAGAAAATTGTTTTCTGTAAACATATTTACA
2161 ---------+---------+---------+---------+---------+---------+---------+ 2220
     TACTACCTGCATCTAAAGTATTCATATATTCATATATTCAGATGTCATGAGAGAGGGTTT
2221 ---------+---------+---------+---------+---------+---------+---------+ 2280
     TGTTCTTGTTCCTGAAAAGCTGGTTTATCATCTGATCAGCATATACTGCGCAACGGGCAG
2281 ---------+---------+---------+---------+---------+---------+---------+ 2340
     GGCTAGAATCCATGAACCAAGCTGCAAAGATCTCACGCTAAATAAGGCGGAAAGATTTGG
2341 ---------+---------+---------+---------+---------+---------+---------+ 2400
     AGAAACGAAAGGAAATTCTTTCCTGTCCAATGTATACTCTTCAGACTAATGACCTCTTCC
2401 ---------+---------+---------+---------+---------+---------+---------+ 2460
     TATCAAGCCTTCTA
2461 ---------+---- 2474
```

Fig. 5 (page 6 of 6)

M-hiap-2

SEQ ID NO:41

```
    CTGTGGTGGAGATCTATTGTCCAAGTGGTGAGAAACTTCATCTGGAAGTTTAAGCGGTCA
  1 ---------+---------+---------+---------+---------+---------+ 60
    GAAATACTATTACTACTCATGGACAkRACTGTCTCCCAGAGACTCGCCCAAGGTACCTTA
 61 ---------+---------+---------+---------+---------+---------+ 120
    CACCCRAAAACTTAAACGTATAATGGAGAAGAGCACAATCTTGTCAAATTGGACAAAGGA
121 ---------+---------+---------+---------+---------+---------+ 180
```

SEQ ID NO:42

```
                          M  E  K  S  T  I  L  S  N  W  T  K  E  -

    GAGCGAAGAAAAAATGAAGTTTGACTTTTCGTGTGAACTCTACCGAATGTCTACATATTC
181 ---------+---------+---------+---------+---------+---------+ 240
     S  E  E  K  M  K  F  D  F  S  C  E  L  Y  R  M  S  T  Y  S  -

    AGCTTTTCCCAGGGGAGTTCCTGTCTCAGAGAGGAGTCTGGCTCGTGCTGGCTTTTATTA
241 ---------+---------+---------+---------+---------+---------+ 300
     A  F  P  R  G  V  P  V  S  E  R  S  L  A  R  A  G  F  Y  Y  -

    TACAGGTGTGAATGACAAAGTCAAGTGCTTCTGCTGTGGCCTGATGTTGGATAACTGGAA
301 ---------+---------+---------+---------+---------+---------+ 360
     T  G  V  N  D  K  V  K  C  F  C  C  G  L  M  L  D  N  W  K  -

    ACAAGGGGACAGTCCTGTTGAAAAGCACAGACAGTTCTATCCCAGCTGCAGCTTTGTACA
361 ---------+---------+---------+---------+---------+---------+ 420
     Q  G  D  S  P  V  E  K  H  R  Q  F  Y  P  S  C  S  F  V  Q  -
```

Fig. 6 (page 1 of 6)

M-hiap-2

```
    GACTCTGCTTTCAGCCAGTCTGCAGTCTCCATCTAAGAATATGTCTCCTGTGAAAAGTAG
421 ---------+---------+---------+---------+---------+---------+ 480
     T  L  L  S  A  S  L  Q  S  P  S  K  N  M  S  P  V  K  S  R  -

    ATTTGCACATTCGTCACCTCTGGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCC
481 ---------+---------+---------+---------+---------+---------+ 540
     F  A  H  S  S  P  L  E  R  G  G  I  H  S  N  L  C  S  S  P  -

    TCTTAATTCTAGAGCAGTGGAAGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCAT
541 ---------+---------+---------+---------+---------+---------+ 600
     L  N  S  R  A  V  E  D  F  S  S  R  M  D  P  C  S  Y  A  M  -

    GAGTACAGAAGAGGCCAGATTTCTTACTTACAGTATGTGGCCTTTAAGTTTTCTGTCACC
601 ---------+---------+---------+---------+---------+---------+ 660
     S  T  E  E  A  R  F  L  T  Y  S  M  W  P  L  S  F  L  S  P  -

    AGCAGAGCTGGCCAGAGCTGGCTTCTATTACATAGGGCCTGGAGACAGGGTGGCCTGTTT
661 ---------+---------+---------+---------+---------+---------+ 720
     A  E  L  A  R  A  G  F  Y  Y  I  G  P  G  D  R  V  A  C  F  -

    TGCCTGTGGTGGGAAACTGAGCAACTGGGAACCAAAGGATTATGCTATGTCAGAGCACCG
721 ---------+---------+---------+---------+---------+---------+ 780
     A  C  G  G  K  L  S  N  W  E  P  K  D  Y  A  M  S  E  H  R  -
```

Fig. 6 (page 2 of 6)

M-hiap-2

```
    CAGACATTTTCCCCACTGTCCATTTCTGGAAAATACTTCAGAAACACAGAGGTTTAGTAT
781 ---------+---------+---------+---------+---------+---------+ 840
     R  H  F  P  H  C  P  F  L  E  N  T  S  E  T  Q  R  F  S  I  -

    ATCAAATCTAAGTATGCAGACACACTCTGCTCGATTGAGGACATTTCTGTACTGGCCACC
841 ---------+---------+---------+---------+---------+---------+ 900
     S  N  L  S  M  Q  T  H  S  A  R  L  R  T  F  L  Y  W  P  P  -

    TAGTGTTCCTGTTCAGCCCGAGCAGCTTGCAAGTGCTGGATTCTATTACGTGGATCGCRA
901 ---------+---------+---------+---------+---------+---------+ 960
     S  V  P  V  Q  P  E  Q  L  A  S  A  G  F  Y  Y  V  D  R  N  -

    TGATGATGTCAAGTGCCTTTGTTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGA
961 ---------+---------+---------+---------+---------+---------+ 1020
     D  D  V  K  C  L  C  C  D  G  G  L  R  C  W  E  P  G  D  D  -

    CCCCTGGATAGAACACGCCAAATGGTTTCCAAGGTGTGAGTTCTTGATACGGATGAAGGG
1021 ---------+---------+---------+---------+---------+---------+ 1080
     P  W  I  E  H  A  K  W  F  P  R  C  E  F  L  I  R  M  K  G  -

    TCAGGAGTTTGTTGATGAGATTCAAGCTAGATATCCTCATCTTCTTGAGCAGCTGTTGTC
1081 ---------+---------+---------+---------+---------+---------+ 1140
     Q  E  F  V  D  E  I  Q  A  R  Y  P  H  L  L  E  Q  L  L  S  -
```

Fig. 6 (page 3 of 6)

M-hiap-2

```
     CACTTCAGACACCCCAGGAGAAGAAAATGCTGACCCTACAGAGACAGTGGTGCATTTTGG
1141 ---------+---------+---------+---------+---------+---------+ 1200
      T  S  D  T  P  G  E  E  N  A  D  P  T  E  T  V  V  H  F  G  -

     CCCTGGAGAAAGTTCGAAAGATGTCGTCATGATGAGCACGCCTGTGGTTAAAGCAGCCTT
1201 ---------+---------+---------+---------+---------+---------+ 1260
      P  G  E  S  S  K  D  V  V  M  M  S  T  P  V  V  K  A  A  L  -

     GGAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTCAGCGGCAGATCCTGGCCAC
1261 ---------+---------+---------+---------+---------+---------+ 1320
      E  M  G  F  S  R  S  L  V  R  Q  T  V  Q  R  Q  I  L  A  T  -

     TGGTGAGAACTACAGGACCGTCAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGA
1321 ---------+---------+---------+---------+---------+---------+ 1380
      G  E  N  Y  R  T  V  N  D  I  V  S  V  L  L  N  A  E  D  E  -

     GAGAAGAGAAGAGGAGAAGGAAAGACAGACTGAAGAGATGGCATCAGGTGACTTATCACT
1381 ---------+---------+---------+---------+---------+---------+ 1440
      R  R  E  E  E  K  E  R  Q  T  E  E  M  A  S  G  D  L  S  L  -

     GATTCGGAAGAATAGAATGGCCCTCTTTCAACAGTTGACACATGTCCTTCCTATCCTGGA
1441 ---------+---------+---------+---------+---------+---------+ 1500
      I  R  K  N  R  M  A  L  E  Q  Q  L  T  H  V  L  P  I  L  D  -
```

Fig. 6 (page 4 of 6)

M-hiap-2

```
     TAATCTTCTTGAGGCCAGTGTAATTACAAAACAGGAACATGATATTATTAGACAGAAAAC
1501 ---------+---------+---------+---------+---------+---------+ 1560
      N  L  L  E  A  S  V  I  T  K  Q  E  H  D  I  I  R  Q  K  T  -

     ACAGATACCCTTACAAGCAAGAGAGCTTATTGACACCGTTTTAGTCAAGGGAAATGCTGC
1561 ---------+---------+---------+---------+---------+---------+ 1620
      Q  I  P  L  Q  A  R  E  L  I  D  T  V  L  V  K  G  N  A  A  -

     AGCCAACATCTTCAAAAACTCTCTGAAGGGAATTGACTCCACGTTATATGAAAACTTATT
1621 ---------+---------+---------+---------+---------+---------+ 1680
      A  N  I  F  K  N  S  L  K  G  I  D  S  T  L  Y  E  N  L  F  -

     TGTGGAAAAGAATATGAAGTATATTCCAACAGAAGACGTTTCAGGCTTGTCATTGGAAGA
1681 ---------+---------+---------+---------+---------+---------+ 1740
      V  E  K  N  M  K  Y  I  P  T  E  D  V  S  G  L  S  L  E  E  -

     GCAGTTGCGGAGATTACAAGAAGAACGAACTTGCAAAGTGTGTATGGACAGAGAGGTTTC
1741 ---------+---------+---------+---------+---------+---------+ 1800
      Q  L  R  R  L  Q  E  E  R  T  C  K  V  C  M  D  R  E  V  S  -

     TATTGTGTTCATTCCGTGTGGTCATCTAGTAGTCTGCCAGGAATGTGCCCCTTCTCTAAG
1801 ---------+---------+---------+---------+---------+---------+ 1860
      I  V  F  I  P  C  G  H  L  V  V  C  Q  E  C  A  P  S  L  R  -
```

Fig. 6 (page 5 of 6)

M-hiap-2

```
     GAAGTGCCCCATCTGCAGGGGGACAATCAAGGGGACTGTGCGCACATTTCTCTCATGAGT
1861 ---------+---------+---------+---------+---------+---------+ 1920
      K  C  P  I  C  R  G  T  I  K  G  T  V  R  T  F  L  S  *     -

     GAAGAATGGTCTGAAAGTATTGTTGGACATCAGAAGCTGTCAGAACAAAGAATGAACTAC
1921 ---------+---------+---------+---------+---------+---------+ 1980
     TGATTTCAGCTCTTCAGCAGGACATTCTACTCTCTTTCAAGATTAGTAATCTTGCTTTAT
1981 ---------+---------+---------+---------+---------+---------+ 2040
     GAAGGGTAGCATTGTATATTTAAGCTTAGTCTGTTGCAAGGGAAGGTCTATGCTGTTGAG
2041 ---------+---------+---------+---------+---------+---------+ 2100
     CTACAGGACTGTGTCTGTTCCAGAGCAGGAGTTGGGATGCTTGCTGTATGTCCTTCAGGA
2101 ---------+---------+---------+---------+---------+---------+ 2160
     CTTCTTGGGATTTGGGAATTTGGGGAAAGCTTTGGAATCCAGTGATGTGGAGCTCAGAAA
2161 ---------+---------+---------+---------+---------+---------+ 2220
     TCCTGGAACCAGTGACTCTGGTACTCAGTAGATAGGGTACCCTGTACTTCTTGGTGCTTT
2221 ---------+---------+---------+---------+---------+---------+ 2280
     TCCAGTCTGGGAAATAAGGAGGAATCTGCTGCTGGTAAAAATTTGCTGGATGTGAGAAAT
2281 ---------+---------+---------+---------+---------+---------+ 2340
     AGATGAAAGTGTTTCGGGTGGGGGCGTGCATCAGTGTAGTGTGTGCAGGGATGTATGCAG
2341 ---------+---------+---------+---------+---------+---------+ 2400
     GCCAAACACTGTGTAG
2401 ---------+------ 2416
```

Fig. 6 (page 6 of 6)

Alignment of BIR (Baculoviral IAP Repeats) Domains

Baculovirus
- Cp_iap — Cydia pomonella
- Op_iap — Orgyia pseudotsugata

Human
- xiap — IAP on X chromosome
- hiap1, hiap2 — two different human IAP genes

Mouse
- m-xiap — mouse homologue of human xiap gene

Insect
- diap — Drosophilia IAP gene, not clearly a homologue of xiap or hiap

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence.

Fig. 7

1 68

SEQ ID NO:11	Op_iap-1	kaaRLgTYtn WPvqf.leps rMAasGFYYl GrgDeVrCaf CkveitnWvr gDdpetdHkr waPqCpFV
SEQ ID NO:14	Cp_iap-1	eevRLnTFek WPvsf.lspe tMAknGFYYl GrsDeVrCaf CkveimrWke gEdpaadHkk waPqCpFV
SEQ ID NO:15	diap-2	eanRLvTFkd WPnpn.iLpq aLAkAGFYYl nrlDhVkCvw CngviakWek nDnafeeHkr ffPqCprV
SEQ ID NO:16	m-xiap-1	efnRLkTFan FPssspvsas tLArAGFLYt GegDtVqCFs ChaaidrWqy gDsavgrHrr isPnCrFI
SEQ ID NO:17	xiap-1	efnRLkTFan FPsgspvsas tLArAGFLYt GegDtVrCFs ChaavdrWqy gDsavgrHrk vsPnCrFI
SEQ ID NO:18	hiap1-1	elyRMsTYst FPagvpvser sLArAGFYYt GvnDkVkCFc CglmldnWkr gDsptekHkk lyPsCrFV
SEQ ID NO:19	hiap2-1	elyRMsTYst FPagvpvser sLArAGFYYt GvnDkVkCFc CglmldnWkl gDspiqkHkq lyPsCsFI
SEQ ID NO:20	m-xiap-2	eeaRLksFqn WPdyahltpr eLAsAGLYYt GadDqVqCFc CggklknWep cDrawseHrr hfPnCfFv
SEQ ID NO:21	xiap-2	eeaRLksFqn WPdyahltpr eLAsAGLLYt GigDqVqCFc CggklknWep cDrawseHrr hfPnCfFV
SEQ ID NO:22	hiap1-2	enaRL1TFqt WP.1Lf1spt dLArAGFYYi GpgDrVaCFa CggklsnWep kDnamseHlr hfPkCpFI
SEQ ID NO:23	hiap2-2	eeaRF1TYhm WP.1Lf1sps eLArAGFYYi GpgDrVaCFa CggklsnWep kDdamseHrr hfPnCpF1
SEQ ID NO:24	m-xiap-3	yeaRivTFgt Wiysv..nke qLArAGFYal GegDkVkCFh CgggltdWkp sEdpwdqHak cyPgCkYl
SEQ ID NO:25	xiap-3	yeaRifTFgt Wiysv..nke qLArAGFYal GegDkVkCFh CgggltdWkp sEdpweqHak wyPgCkYl
SEQ ID NO:26	hiap1-3	haaRFkTFfn WPssvlvnpe qLAsAgFYYv GnsDdVkCFc CdgglrcWes gDdpwvqHak wfPrCeYl
SEQ ID NO:27	hiap2-3	haaRMrTFmy WPssvpvqpe qLAsAGFYYv GrnDdVkCFg CdgglrcWes gDdpwveHak wfPrCeF1
SEQ ID NO:28	Op_iap-2	eaaRLrTFae WPrglkqrpe eLAeAGFFYt GqgDktrCFc CdgglkdWep dDapwqqHar wydrCeYV
SEQ ID NO:29	Cp_iap-2	eaaRvksFhn WPrcmkqrpe qMAdAGFFYt GygDntkCFy CdgglkdWep eDvpweqHvr widrCaYV
SEQ ID NO:30	diap-3	vdaRLrTFtd WPisniqpas aLAqAGLYYq kigDqVrCFh CniglrsWqk eDepwieHak wsPkCqFV
SEQ ID NO:31	diap-1	esvRLaTFge WPlnapvsae dLvanGFF.. GtwmeaeCdf ChvridrWey gDlvaerHrr ssPiCsmV
SEQ ID NO:2	Consensus	---RL-TF-- WP-------- -LA-AGFYY- G--D-V-CF- C------W-- -D-----H-- --P-C-FV

```
                                1                                                                                50
SEQ ID NO:12        cp-iap ..........  ..........  ..........  ..........  ..........  ..........
SEQ ID NO:13          diap ..........  ..........  mtelgMelEs  vRLaTFgeWP  lnaPVSaedL
SEQ ID NO:10      m-xiap   ...mtfnsfe  gtrtfvladt  nkdeEFveEF  nRLkTFanFP  sssPVSastL
SEQ ID NO:4         xiap   ...mtfnsfe  gsktcvpadi  nkeeEFveEF  nRLkTFanFP  sgsPVSastL
SEQ ID NO:6       hiap1    mnivensifl  snlmksantf  elkyDLscEL  yRMsTYstFP  agvPVSersL
SEQ ID NO:8       hiap2    ...medstil  sdwtns.nkq  kmkyDFscEL  yRMsTYstFP  agvPVSersL
SEQ ID NO:44  consensus    ----------  ----------  -----F--E-  -RL-TF--FP  ---PVS---L

                               51                BIR 1                                                          100
                    cp-iap ..........  ..........  ..........  ..........  ..........
                      diap vanGFFaTGk  wleaeChfCh  vriDrWeyGD  qvaerHrrss  PiCsmVla..
                    m-xiap ARAGFLYTGe  gDtVqCFsCh  aaiDrWqyGD  SavgrHrris  PnCrFIngFy
                      xiap ARAGFLYTGe  gDtVrCFsCh  aavDrWqyGD  SavgrHrkvs  PnCrFIngFy
                     hiap1 ARAGFYYTGv  nDkVkCFcCg  lmlDnWkrGD  SptekHkkly  PsCrFVqsLn
                     hiap2 ARAGFYYTGv  nDkVkCFcCg  lmlDnWklGD  SpiqkHkqly  PsCsFIqnLV
                consensus ARAGF-YTG-  -D-V-CF-C-  ---D-W--GD  S----H----  P-C-FI----

                               101                                                                              150
                    cp-iap ..........  ..........  ..........  ..........  ..........
                      diap ..........  ..........  ..........  ..........P nhcgnvprsq
                    m-xiap ..........  ......feng  aaqStnpgiq  ngqyksenCv  gnrnpfapdR
                      xiap ..........  ......lens  atqStnsgiq  ngqykvenYl  gsrdhfaldR
                     hiap1 svnnleatsq  ptfpssvths  .thSllpgte  nsgyfrgsYs  nspsnpvnsR
                     hiap2 s.aslgstsk  nt..spmrns  fahSlsptle  hsslfsgsYs  slppnplnsR
                consensus ----------  ----------  ---S------  --------Y-  ---------R
```

Fig. 8 (page 1 of 5)

```
                151                                                                                                200
cp-iap  ..........  .......mSD lrl.......  ..EEvRLnTF ekWPv.sfLs
  diap  esDnegnsvv dspescscpD lll.......  ..EanRLvTF kdWPn.pnit
m-xiap  ppEthadyll rtgqvvDiSD tiyprnp.aM  csEEARLksF qnWPdyahLt
  xiap  psEthadyll rtgqvvDiSD tiyprnp.aM  ycEEARLksF qnWPdyahLt
 hiap1  anq.......  ......EfSa lmrssypcpM  nnEnARLlTF qtWP.ltfls
 hiap2  avE.......  ......DiSs srtnpysyaM  stEEARFlTY hmWP.ltfLs
consensus --E-------  ------D-SD ---------M  --EEARL-TF --WP----L-

                                BIR 2
                201                                                                                                250
cp-iap  PetMAknGFY YlGrsDeVrC afCkveimrW  kegEdpaaDH kkwaPqCPFV
  diap  PqaLakAGFY YlnrlDhVkC vwCnGviakW  EknDnAfeEH kRfFPqCPrV
m-xiap  PrELAsAGLY YtGadDqVqC FcCGGKLkNW  EPcDrAwSEH rRHFPnCfFV
  xiap  PrELAsAGLY YtGigDqVqC FcCGGKLkNW  EPcDrAwSEH rRHFPnCfFV
 hiap1  PtDLArAGFY YiGpgDrVaC FaCGGKLsNW  EPkDnAmSEH lRHFPkCPFI
 hiap2  PsELArAGFY YiGpgDrVaC FaCGGKLsNW  EPkDdAmSEH rRHFPnCPFl
consensus P-ELA-AGFY Y-G--D-V-C F-CGGKL-NW  EP-D-A-SEH -RHFP-CPFV

                                                                BIR 3
                251                                                                                              300
cp-iap  kgidvcgsiv ttnniqnttt hdtiigPahP  kyAheaARvk sFhnWPrcmk
  diap  qmgplie.fa tgknldelgi qpttl.PlrP  kyAcvdARlr TftdWPiSnI
m-xiap  lgrnvnvrse s.gvssdrnF pnStnsPrNP  aMAeyeARiv TFgtWiyS..
  xiap  lgrnlnirse sdavssdrnF pnStnlPrNP  sMAdyeARif TFgtWiyS..
 hiap1  ..........  enqlqdtsrY tvS.....Nl  sMqthaARfk TFfnWPsSvl
 hiap2  ..........  ensl.etlrF siS.....Nl  sMqthaARmr TFmyWPsSvp
consensus ----------  ---------F --S---P-NP  -MA-[--AR--] TF--WP-S--
```

Fig. 8 (page 2 of 5)

BIR 3

```
                301                                                      350
cp-iap     qrpEQMAdAG FFYtGyGDnt KCFyCdGGLk dWepeDvPWe QHvrWFdrCa
  diap     qpasaLAqAG LYYqkiGdqv rCFhCniGLr sWqkeDEPWf eHAKWsPkCq
m-xiap     VnkEQLArAG FYalGeGDkV KCFhCgGGLt dWkpsEDPWd QHAKcYPgCk
  xiap     VnkEQLArAG FYalGeGDkV KCFhCgGGLt dWkpsEDPWd QHAKWYPgCk
 hiap1     VnpEQLAsAG FYYvGnsDdV KCFcCdGGLr cWesgDDPWv QHAKWFPrCe
 hiap2     VqpEQLAsAG FYYvGRsDdV KCFgCdGGLr cWesgDDPWv eHAKWFPrCe
consensus  V--EQLA-AG FYY-G-GD-V KCF-C-GGL- -W---DDPW- QHAKWFP-C-

                351                                                      400
cp-iap     Yvqlv KGrDY VqkVit.... ..........  ....e.....  ..........
  diap     Fvlla KGpaY VseVlattaa nassqpaTap  aptlq.....  ..........
m-xiap     YLlde KGQEY InnIhlthp. LeEsLgrTae  kt........  .....Ppltk
  xiap     YLleq KGQEY InnIhlths. LeEcLvrTte  kt........  .....Psltr
 hiap1     YLiri KGQEY IrqVqasyph L1EqL1sTsD  spgdenaess  iihlePgedh
 hiap2     FLirm KGQEF VdeIqgryph L1EqL1sTsD  ttgeenadpp  iihfgPgess
consensus  YL---KGQEY ----------  L-E-L--T--  ----------  -----P----

                401                                                      450
cp-iap     ..acVLpge. ..........  ..........  ..........  ..........
  diap     ..adVLmdea pakeAltLGi  dggvVrnaiq  rK1issGcaF  st1deL1hDi
m-xiap     kiDdtifqnP mVqeAirMGF  sfkdlKktme  eKIqtsGssY  lslevLIaDL
  xiap     riDdtifqnP mVqeAirMGF  sfkdIKkime  eKIqisGsnY  kslevLVaDL
 hiap1     seDaIMmntP vInaAveMGF  srslVKqtvq  rKIlatGenY  rlvndLVlDL
 hiap2     seDaVMmntP vVksAleMGF  nrdlVKqtvl  sKIlttGenY  ktvndiVsaL
consensus  --D-V----P -V--A--MGF  ----VK----  -KI---G--Y  -----LV-DL
```

Fig. 8 (page 3 of 5)

```
           451                                                        500
cp-iap     .......... .......... .......... .......... ..........
diap       fddagagaal Evreppe... .......... .......... ..........
m-xiap     vsAqkDnteD E......... .......... .......... ..........
xiap       vnAqkDsmqD E......... .......... .......... ..........
hiap1      lnAedEireE Ererateeke sndlllirkn rmalfqhltc vipildsllt
hiap2      lnAedEkreE Ekekqaeema sddlslirkn rmalfqqltc vlpildnllk
consensus  --A------- E--------- ---------- ---------- ----------

           501                                                        550
cp-iap     .......... .......... ..nttvstaa pvsepipe.. ..........
diap       .......... ...psapfie pcqattskaa svpipvadsi pakpqaaeav
m-xiap     .......... ....ssQtsL Q......... .......... ..........
xiap       .......... ....ssQtsL Q......... .......... ..........
hiap1      agiineqehd vikqktQtsL Qarelidtil vkgniaatvf rnslqeaeav
hiap2      anvinkqehd iikqktQipL Qarelidtiw vkgnaaanif knclkeidst
consensus  ---------- ------Q--L Q--------- ---------- ----------
```

Fig. 8 (sheet 4 of 5)

Ring Zinc Finger

```
          551                                                        600
cp-iap  ...tki.... .......... .....Ekepq veDskLCKIC yveEciVcFV
  diap  sniskitdei qkmsvstpng nlSlEEenRq LkDarLCKVC LDeEVgVVFl
m-xiap  .......... .........k diStEEQLRR LqEEkLsKIC MDrnIaIVFf
  xiap  .......... .........k eiStEEQLRR LqEEkLCKIC MDrnIaIVFV
 hiap1  lyehlfvqqd ikyiptedvs dlpvEEQLRR LpEErtCKVC MDkEVsIVFI
 hiap2  lyknlfvdkn mkyiptedvs glSlEEQLRR LqEErtCKVC MDkEVsVVFI
consensus ---------- ---------- --S-EEQLRR L-EE-LCK-C MD-EV--VF-

          601                                                  635
cp-iap  PCGHvVaCak CAlSVdKCPM CRkIVtsvlk vYFS.
  diap  PCGHLatCnq CApSVanCPM CRadIkgfvr tFLS*
m-xiap  PCGHLatCkq CAeaVdKCPM CytVItfnqk iFMS*
  xiap  PCGHLVtCkq CAeaVdKCPM CytVItfkqk iFMS*
 hiap1  PCGHLVvCkd CApSlrKCPi CRstIkgtvr tFLS*
 hiap2  PCGHLVvCqe CApSlrKCPi CRgIIkgtvr tFLS.
consensus PCGHLV-C-- CA-SV-KCPM CR--I----- -FLS-
```

Fig. 8 (sheet 5 of 5)

Alignment of RZF (Ring Zinc Finger) Domains

Baculovirus
- Cp_iap — Cydia pomonella
- Op_iap — Orgyia pseudotsugata

Human
- xiap — IAP on X chromosome
- hiap1, hiap2 — two different human IAP genes

Mouse
- m-xiap — mouse homologue of human xiap gene

Insect
- diap — Drosophilia IAP gene, not clearly a homologue of xiap or hiap

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

```
                                1                                          46
SEQ ID NO:32 hiap2      EqlrrlqEer tCKVCMdkev sVvFiPCGHl vvCqeCApel rkCPiC
SEQ ID NO:33 hiap1      EqlrrlpEer tCKVCMdkev sIvFiPCGHl w CkdCApsl rkCPiC
SEQ ID NO:34 m-xiap     EqlrrlqEek lsKICMdrni aIvFfPCGHl atCkqCAeav dkCPmC
SEQ ID NO:35 xiap       EqlrrlqEek lCKICMdrni aIvFvPCGHl vtCkqCAeav dkCPmC
SEQ ID NO:36 diap       EenrqlkDar lCKVCLdeev gVvFlPCGHl atCnqCApev anCPmC
SEQ ID NO:37 Cp_iap     EkepgveDsk lCKICyveec iVcFvPCGHv vaCakCAlsv dkCPmC
SEQ ID NO:38 Op_iap     aveaevaDdr lCKICLgack tVcFvPCGHv vaCgkCAagv ttCPvC
SEQ ID NO:1  consensus  E------E-- -CKICM---- -V-F-PCGH- --C--CA--- --CP-C
```

Fig. 9

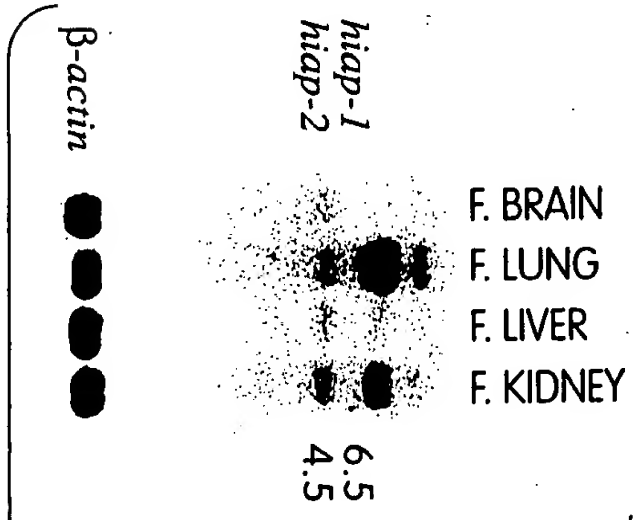

Fig. 10C

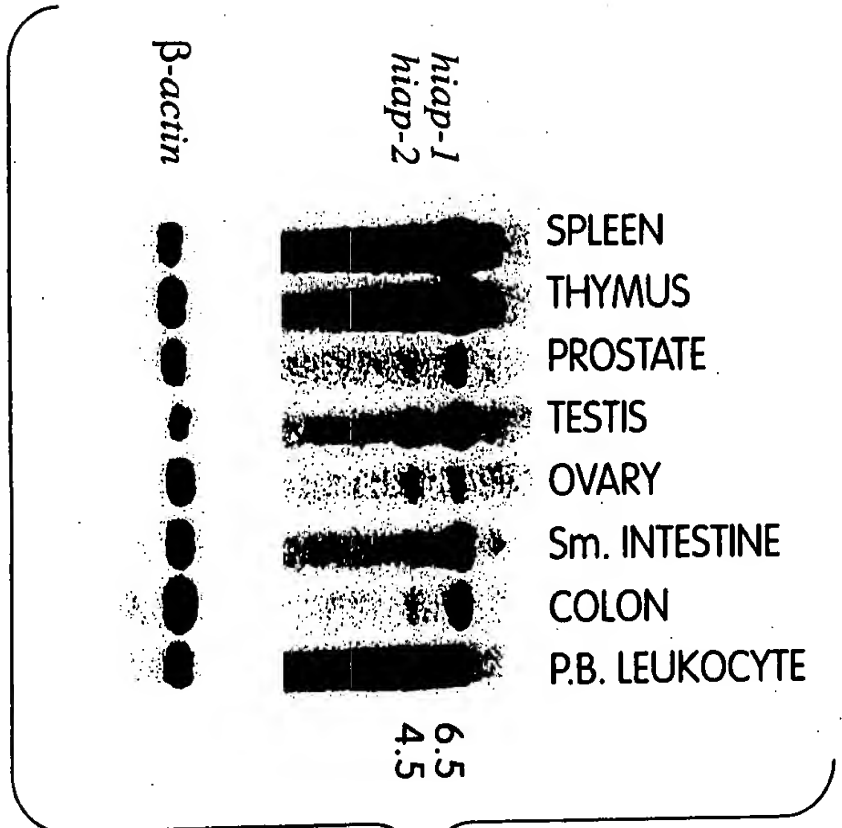

Fig. 10B

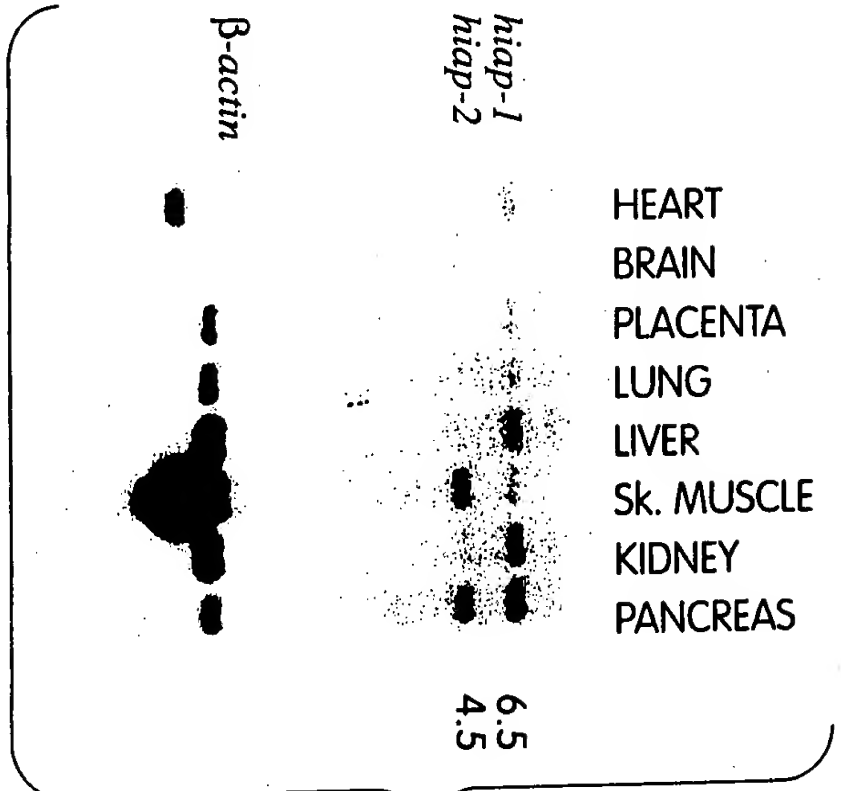

Fig. 10A

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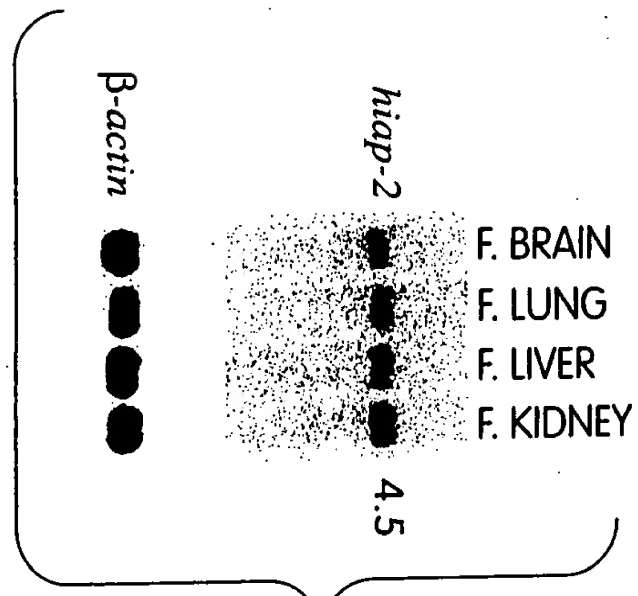

Fig. 11C

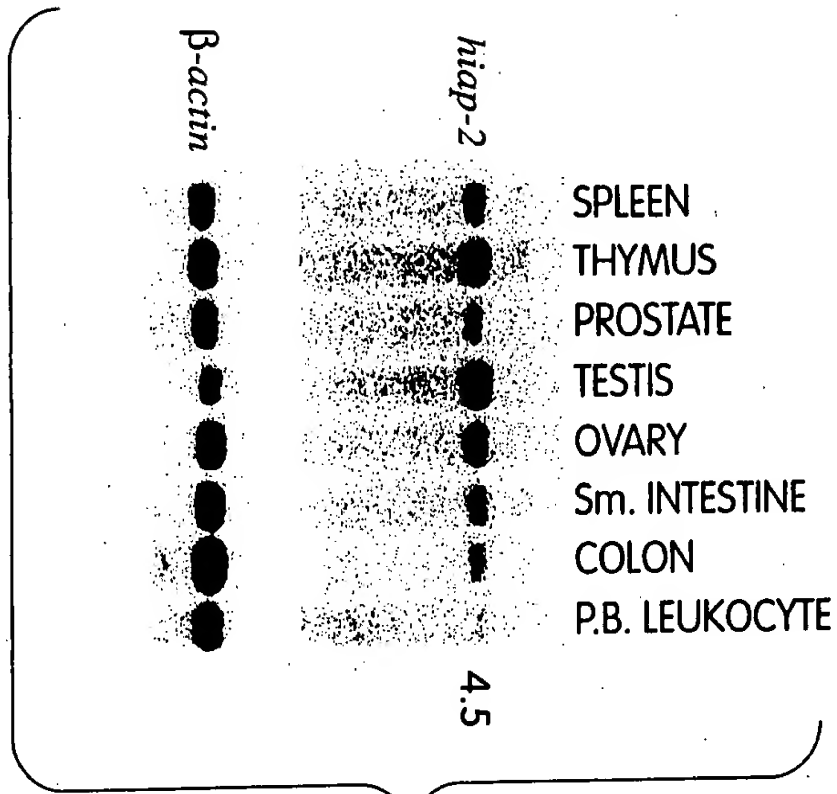

Fig. 11B

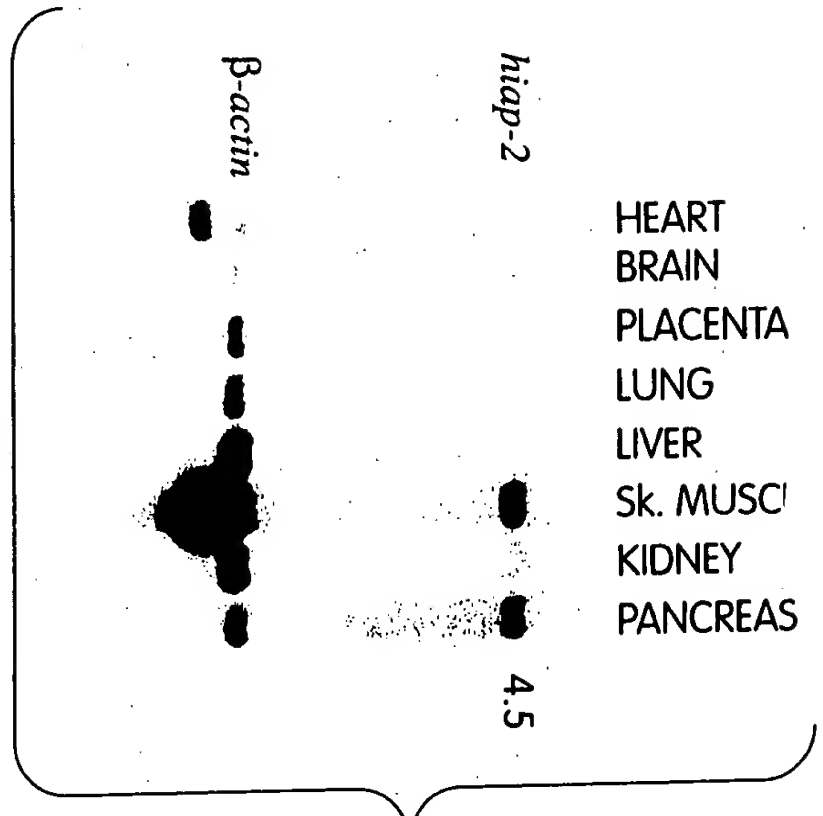

Fig. 11A

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Fig. 12A

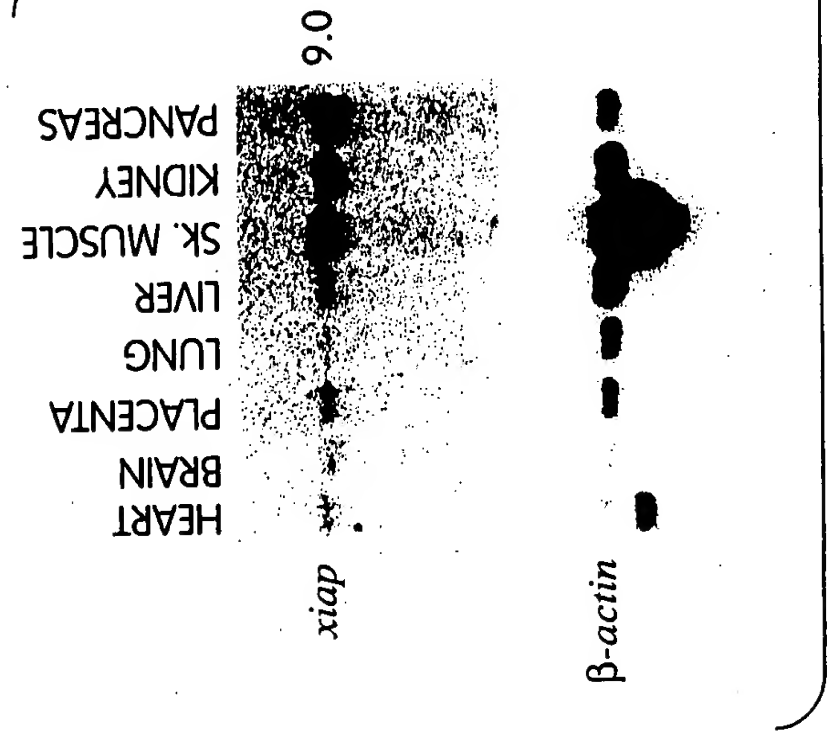


Fig. 12B

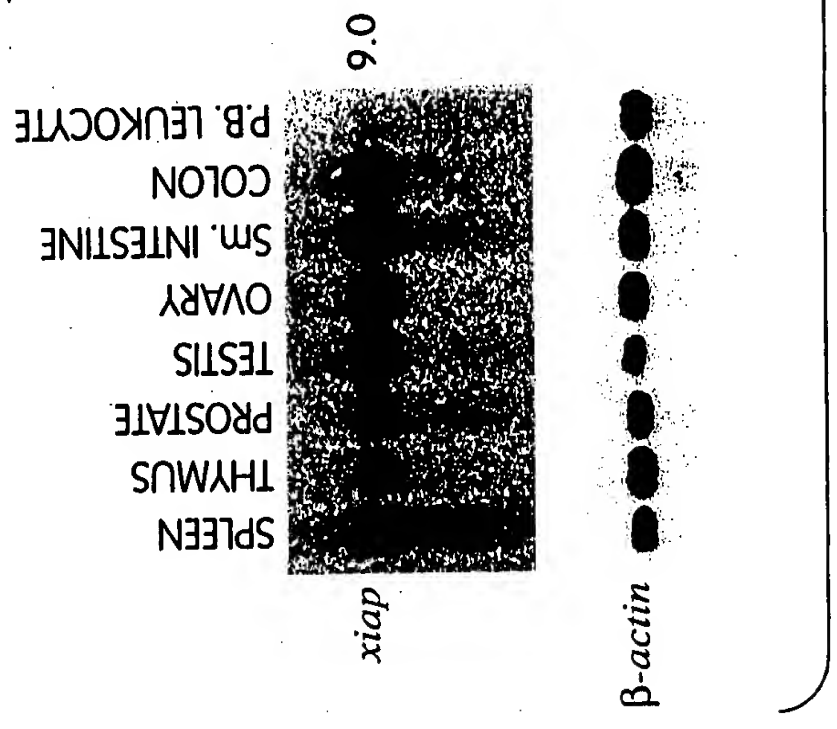
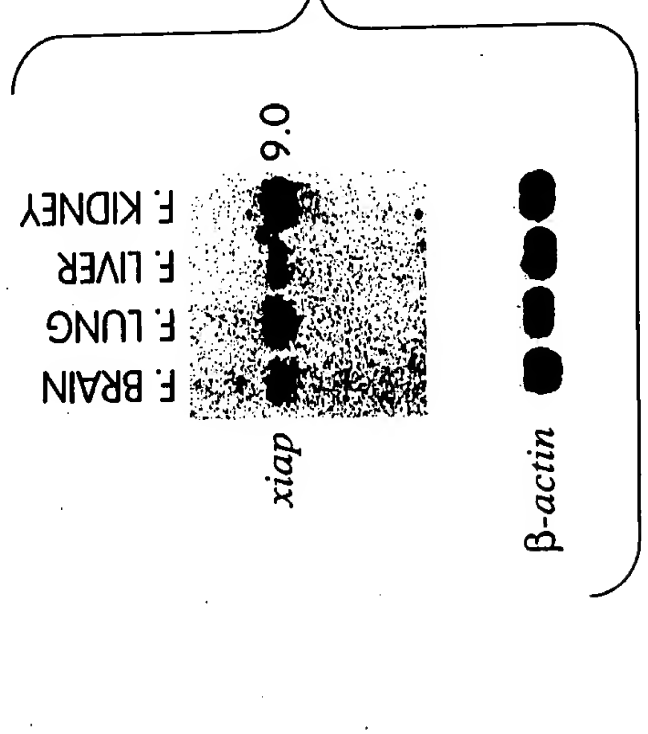


Fig. 12C



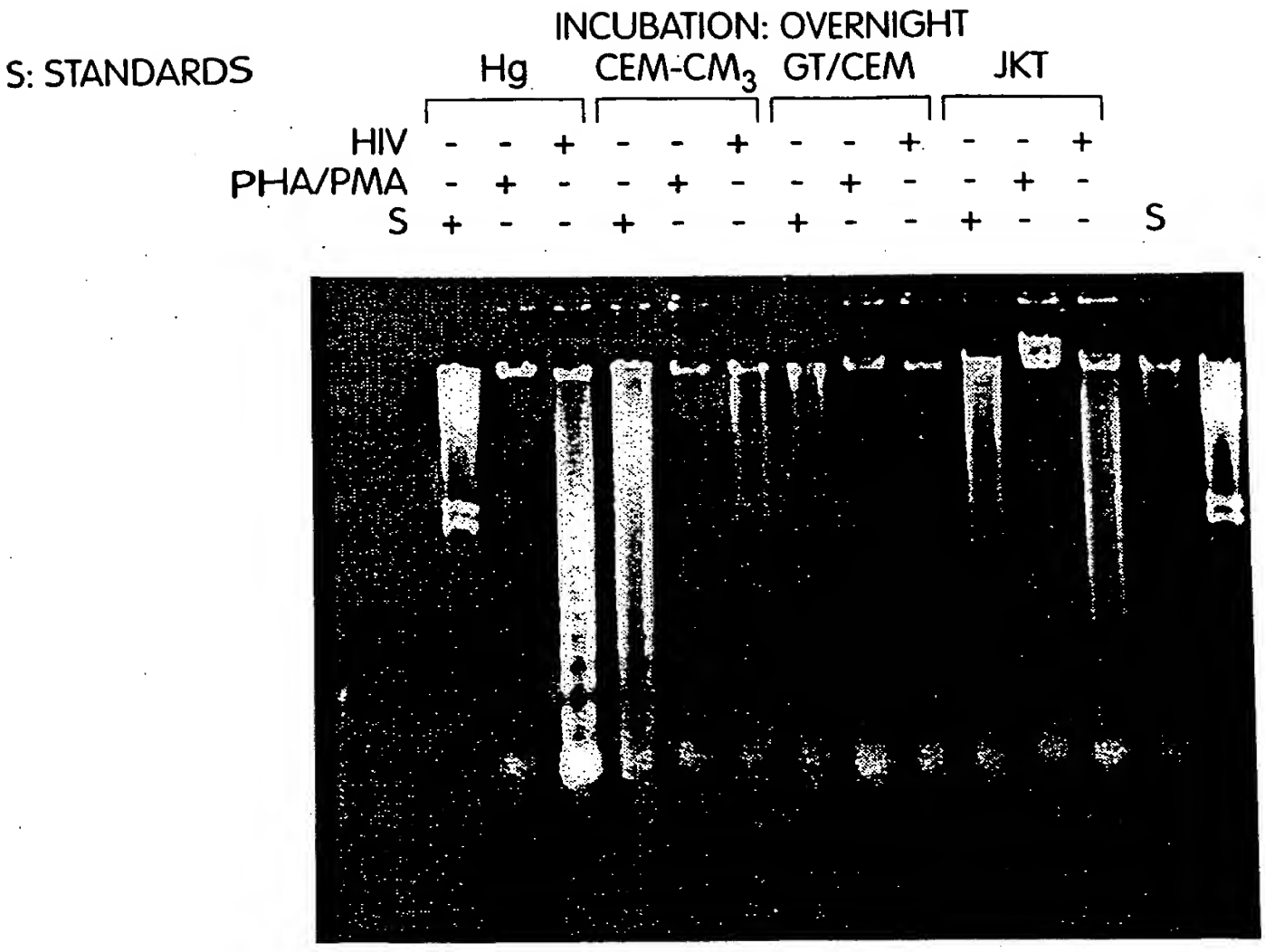


Fig. 13A

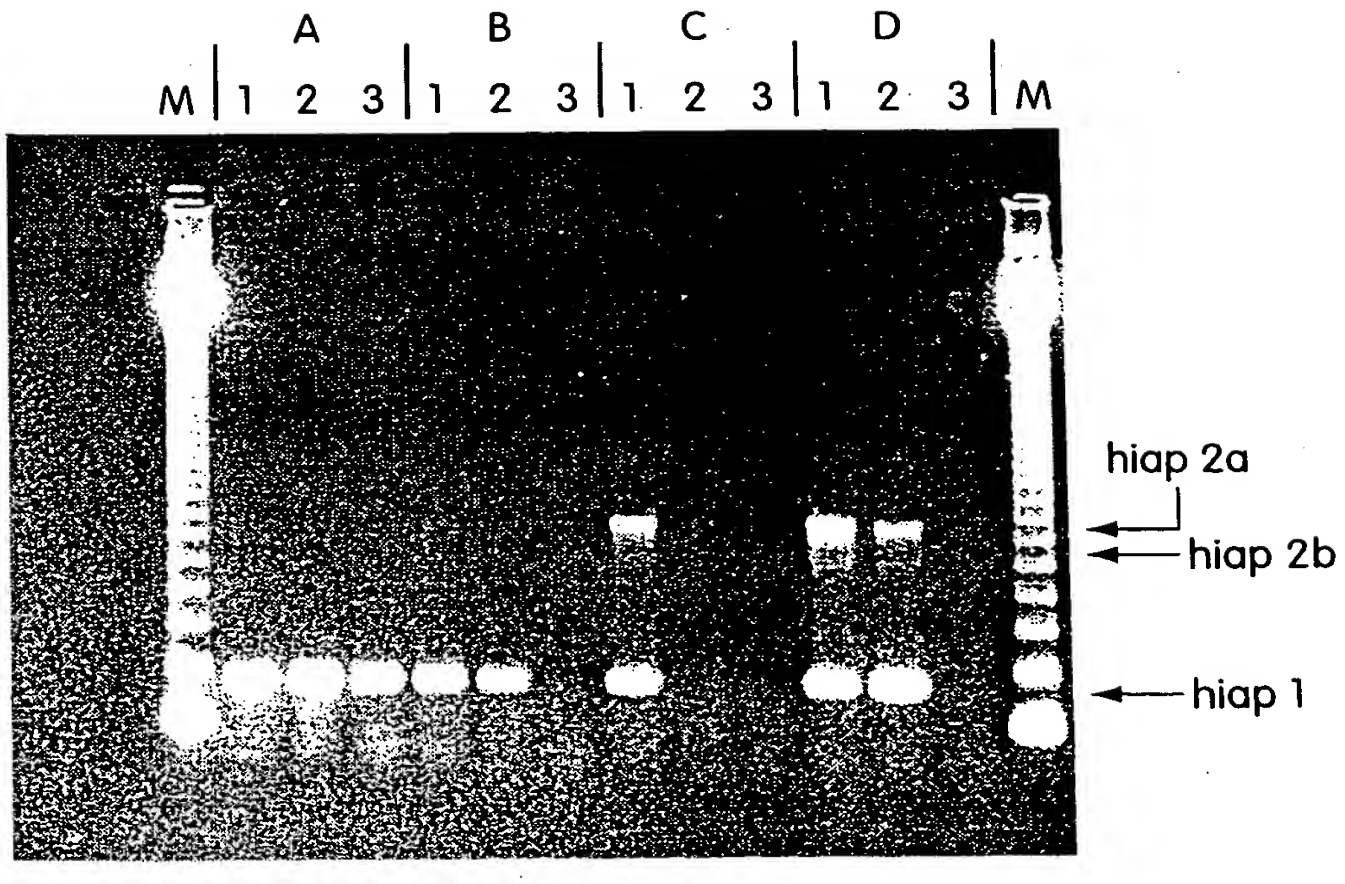


Fig. 13B

BEST AVAILABLE COPY

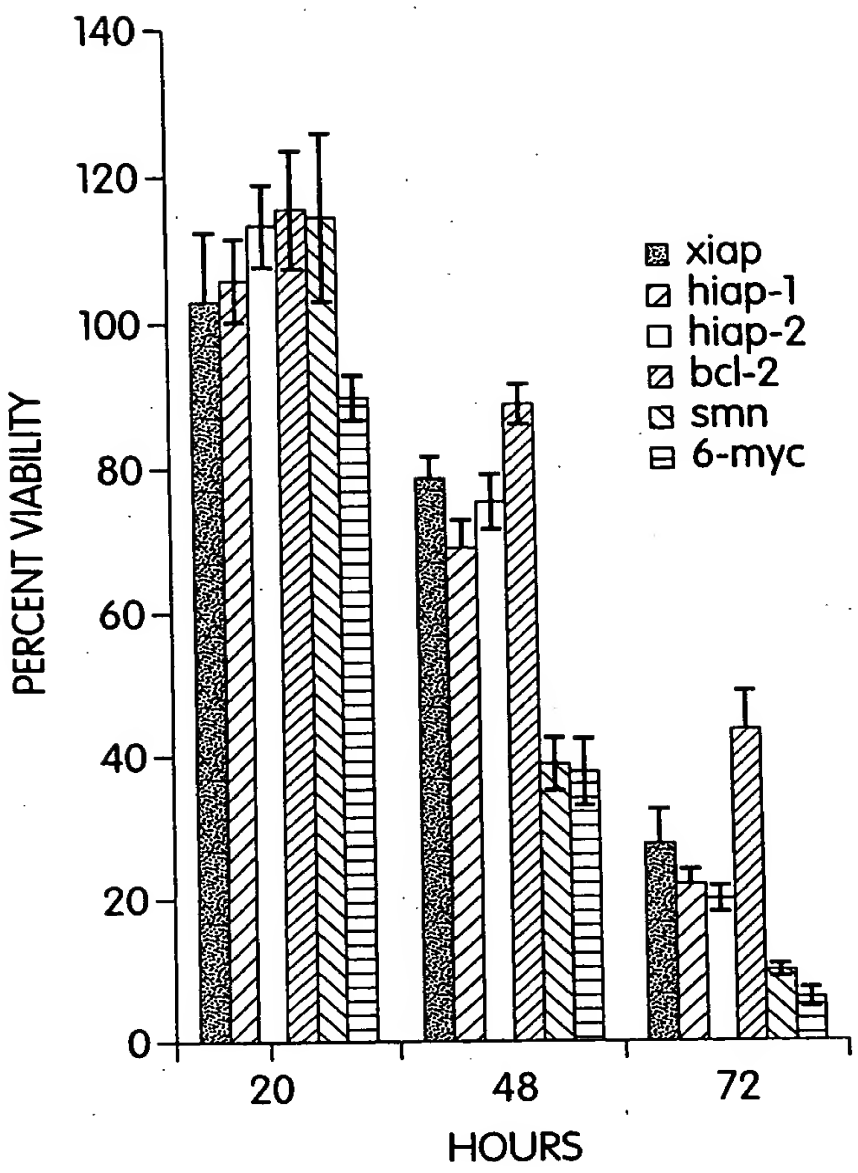


Fig. 14A

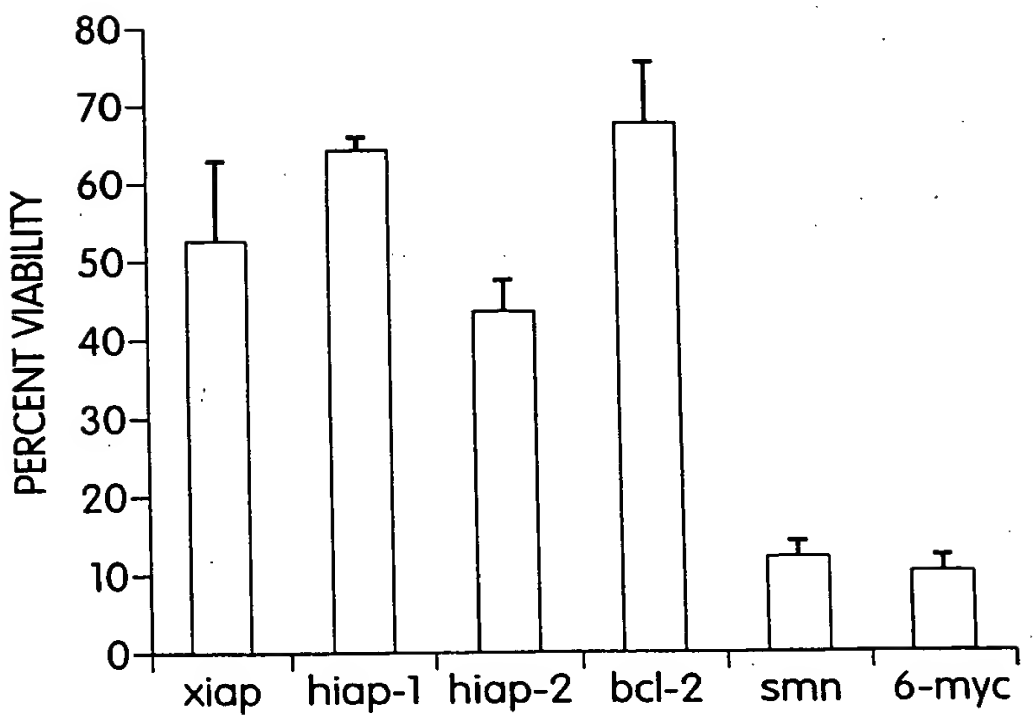


Fig. 14B

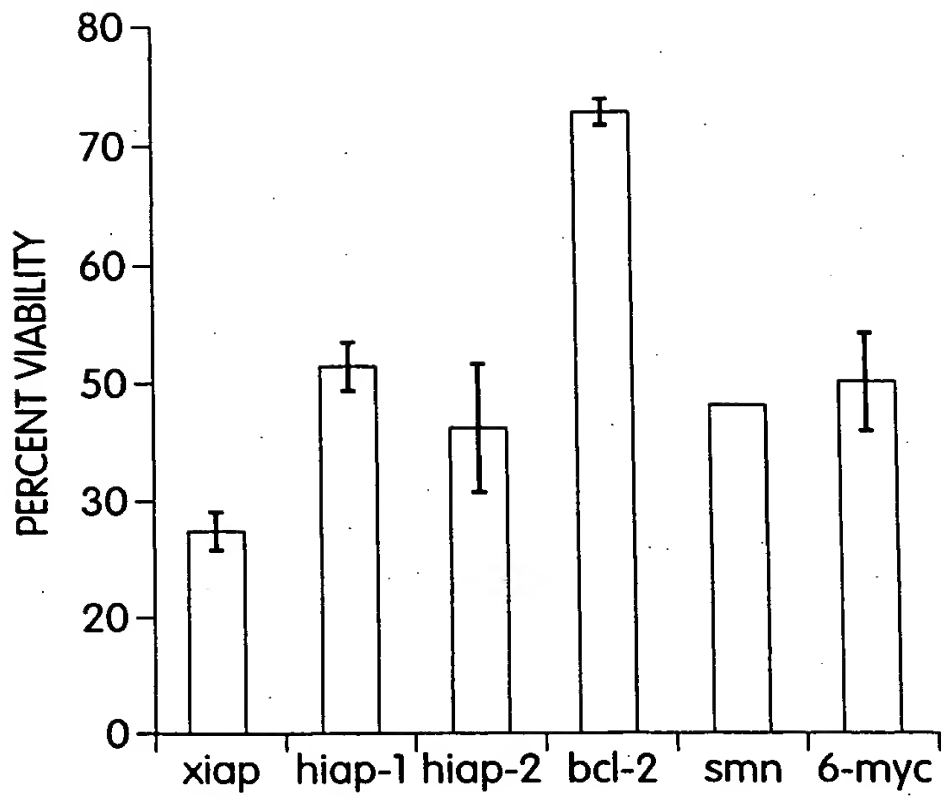


Fig. 14C

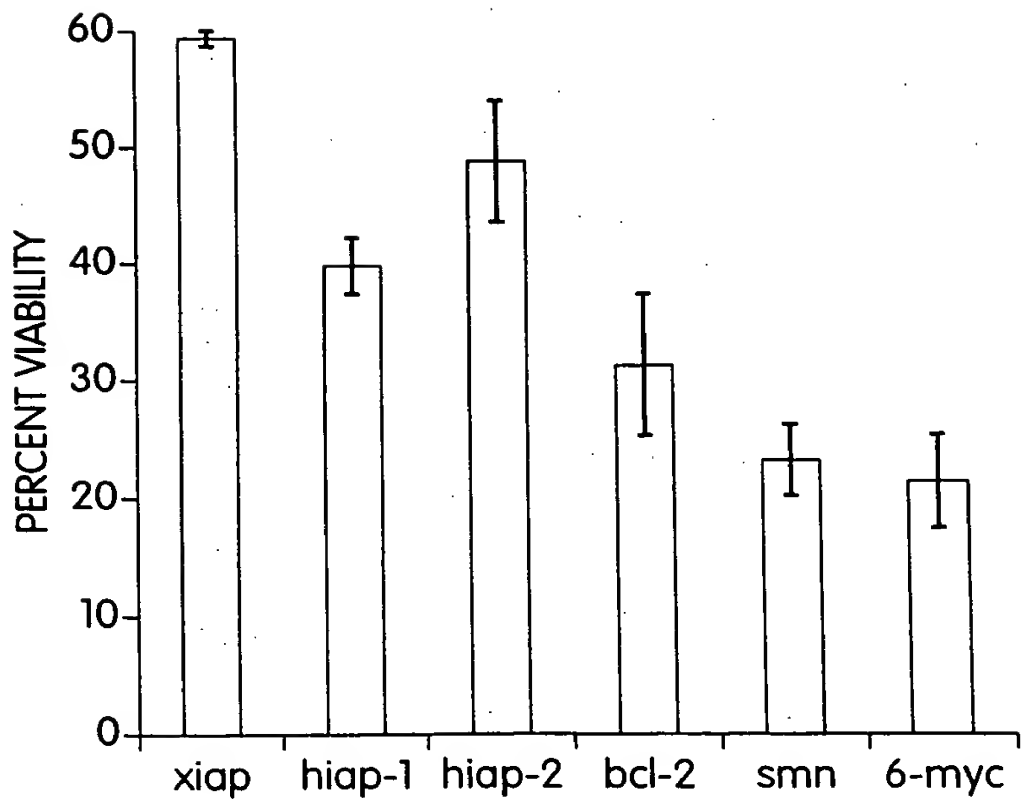


Fig. 14D